

## FIGURE 1A

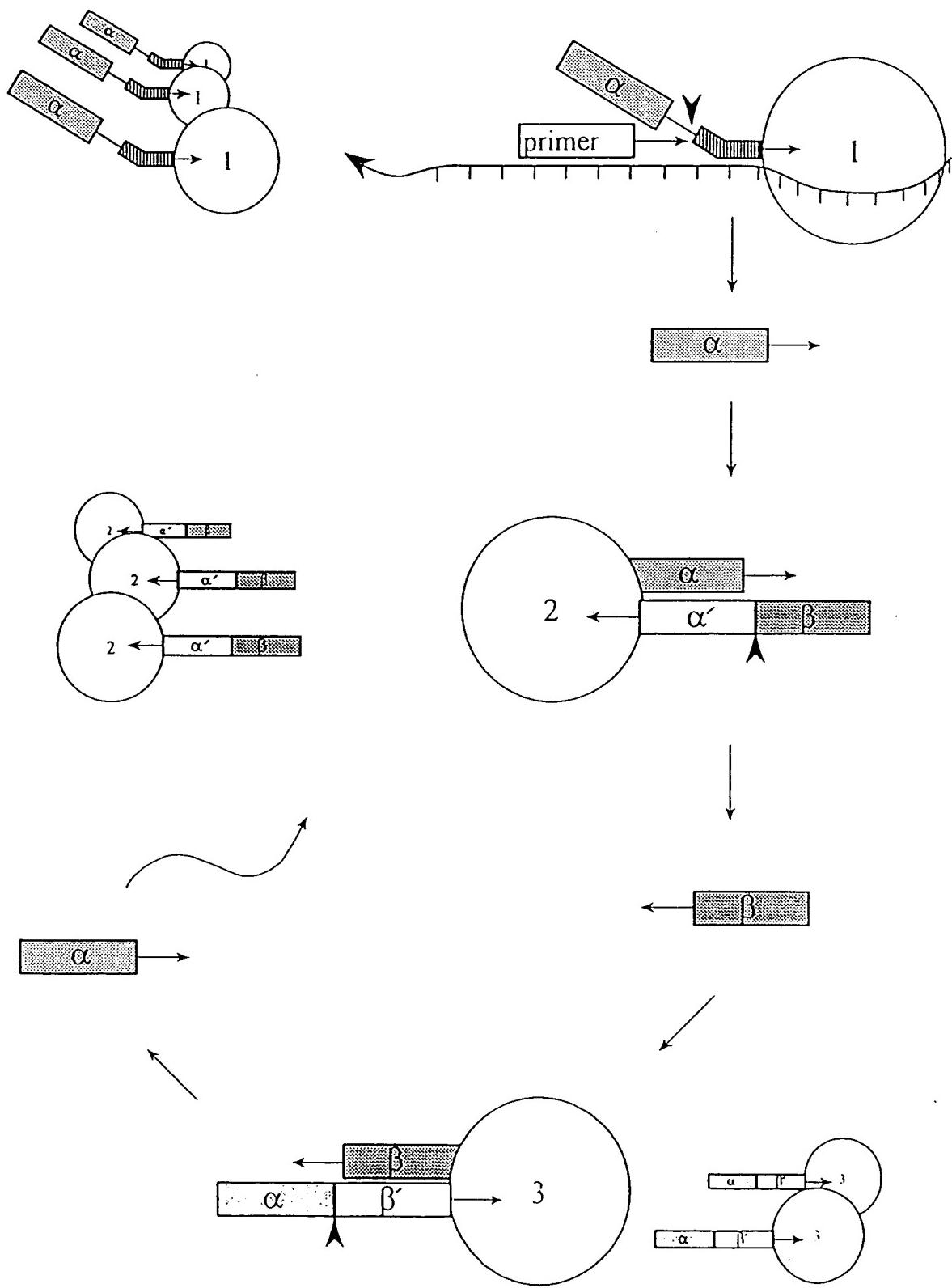
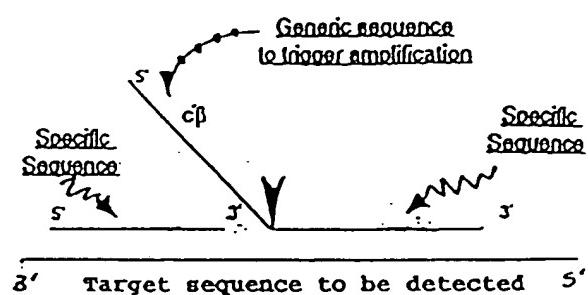
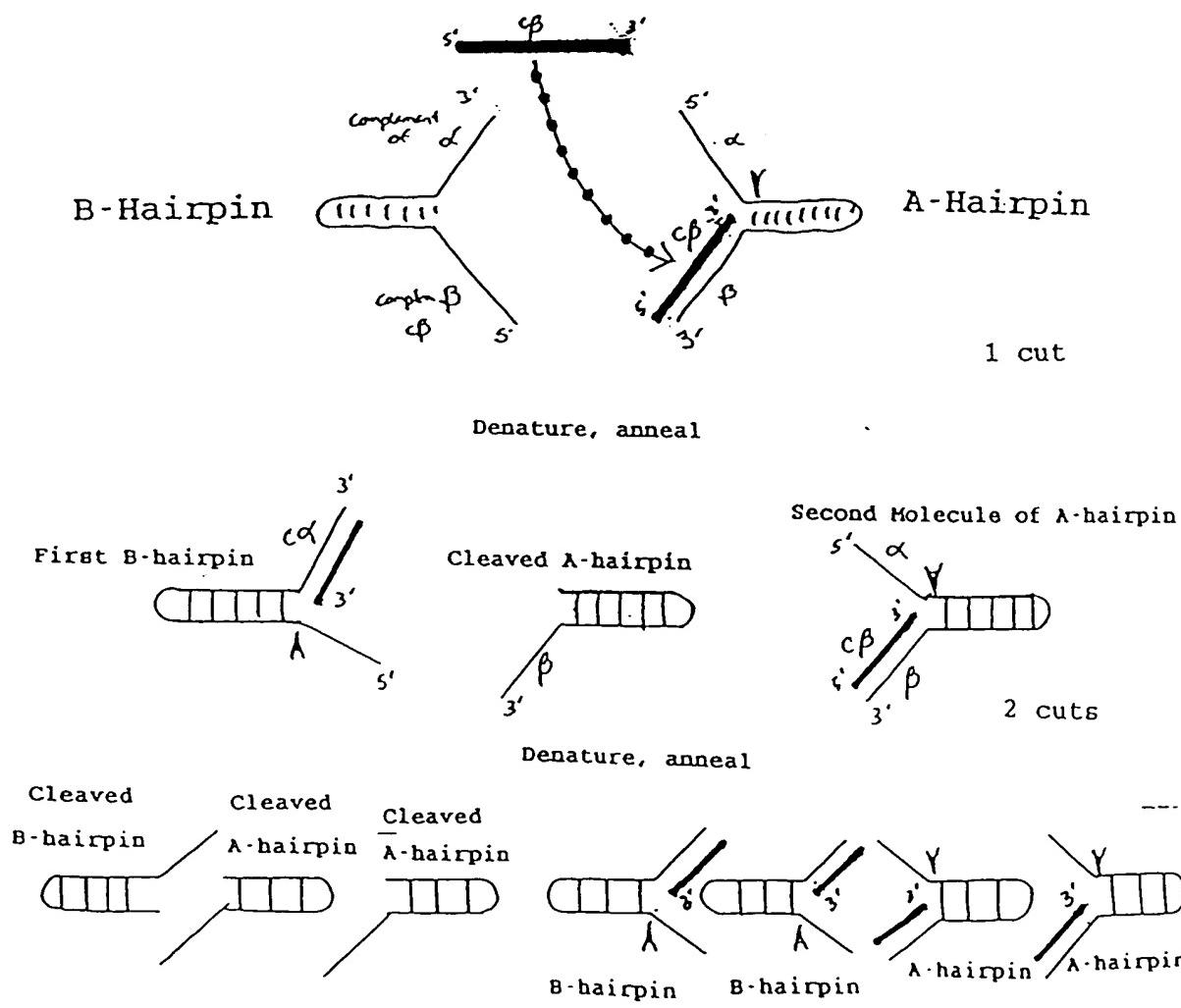


FIGURE 1B

PART ONE: TRIGGER REACTION



PART TWO: DETECTION REACTION



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FIGURE 2

FIGURE 2 (cont'd)

FIGURE 2 (cont'd)

| MAJORITY (SEQ ID NO:7) | TCAGGGCACATGGAXGACCTGAXGCTCTGGAGCTTCCCACGTGCCAACCTGGCCCTGGAA         | 764  |
|------------------------|--|------|
| DNAPTAQ (SEQ ID NO:1)  | T.....C.....A.....T.....A.....A.....C.....G.....A.....               | 761  |
| DNAPTR                 | .....GGG.....G.....C.....GGC.....T.....C.....A.....T.....A.....      | 761  |
| DNAPTH                 | A.....C.....A.....C.....G.....T.....C.....G.....C.....               | 770  |
| MAJORITY               | GGTGCACTTCCCCAAGXGGGGGAGCCCCAACCGGGGAGGGCTTACGGCCCTTCTGGAGAGCTGGACTT |      |
| DNAPTAQ                | .....AA.....A.....T.....A.....T.....T.....GC.....T.....T.....        | 834  |
| DNAPTR                 | .....GG.....G.....C.....CACA.....A.....T.....T.....GC.....T.....     | 831  |
| DNAPTH                 | .....C.....C.....G.....G.....G.....G.....G.....C.....                | 840  |
| MAJORITY               | GGCAGCCTCCCTCAGGAGTTGGGCTCCTGACCCCCAAGCCCCCTGGAGGAGCCCCCTGGCCCC      |      |
| DNAPTAQ                | .....T.....AA.....A.....G.....G.....GGCA.....                        | 904  |
| DNAPTR                 | .....A.....G.....G.....GGCA.....                                     | 901  |
| DNAPTH                 | .....C.....C.....GGCG.....   | 910  |
| MAJORITY               | CGCAAGGGCCCTCGTGGCTTTCGCTTCCCCGAGCCCCATGTCGAGCTTCTGGCCCTGGCC         |      |
| DNAPTAQ                | .....G.....AAG.....AAG.....  | 974  |
| DNAPTR                 | .....T.....T.....TC.....T.....                                       | 971  |
| DNAPTH                 | .....C.....C.....G.....AAA.....                                      | 980  |
| MAJORITY               | CCCCCAGGGAGCCCCCTCACCCCCACCAAGACCCCTTAXGGCCCTXAGGGACCTXAGGGAGCTG     |      |
| DNAPTAQ                | .....G.....G.....G.....T.....A.....AA.....G.....                     | 1044 |
| DNAPTR                 | .....G.....CC.....T.....A.....C.....G.....                           | 1041 |
| DNAPTH                 | .....T.....G.....G.....GGC.....G.....A.....                          | 1050 |

FIGURE 2 (cont'd)

|                      |               |   |      |
|----------------------|---------------|---|------|
| MAJORITY             | (SEQ ID NO:7) | CGGGGXXCTCCTCCCCAAGGACCTGGCCGTTCGGCCCTGAGGAAGGGCTXGACCTCTGCCGCCGACG   |      |
| D <sub>4</sub> APTRQ | (SEQ ID NO:1) | .....G.....T.....A.....AG.....C.....A.....T.....G.....CC.....C.....   | 1111 |
| D <sub>4</sub> APTR  | (SEQ ID NO:2) | .....AA.....G.....G.....C.....C.....G.....T.....C.....A.....A.....    | 1120 |
| D <sub>4</sub> APTH  | (SEQ ID NO:3) | .....C.....C.....C.....C.....T.....G.....A.....G.....                 |      |
| <b>MAJORITY</b>      |               |   |      |
| D <sub>4</sub> APTRQ |               | ACCCCATGGCTCCGCCTAACCTCTGACCCCTCCAAACACCACCCCCACGGGCTGGCCCCGGCTAACCC  |      |
| D <sub>4</sub> APTR  |               | .....G.....T.....T.....T.....T.....T.....T.....T.....T.....           | 1184 |
| D <sub>4</sub> APTH  |               | .....G.....T.....T.....T.....T.....T.....T.....T.....T.....           | 1181 |
| <b>MAJORITY</b>      |               |   |      |
| D <sub>4</sub> APTRQ |               | GGGGGAGTGACGGAGGAXGGCTTCCTCTCCAGAGGCTCTTCCTXGAACCTXXXGGAG             |      |
| D <sub>4</sub> APTR  |               | .....G.....T.....A.....GG.....G.....C.....A.....AAA.....              | 1254 |
| D <sub>4</sub> APTH  |               | .....C.....C.....CCC.....C.....C.....G.....CAT.....G.....CCTTA.....   | 1251 |
| <b>MAJORITY</b>      |               |   |      |
| D <sub>4</sub> APTRQ |               | GGCCCTTAGGGGAGGAGGCTCTTGGCTTACAGGAGGTGGAGAAGCCCCTTCCCGCTCCCTGG        |      |
| D <sub>4</sub> APTR  |               | .....A.....G.....A.....AC.....C.....G.....G.....A.....A.....          | 1260 |
| D <sub>4</sub> APTH  |               | .....C.....C.....A.....C.....A.....C.....C.....                       |      |
| <b>MAJORITY</b>      |               |   |      |
| D <sub>4</sub> APTRQ |               | A.G.....A.....A.....AC.....C.....G.....G.....A.....A.....             | 1324 |
| D <sub>4</sub> APTR  |               | .....G.....G.....G.....A.....C.....C.....T.....T.....                 | 1321 |
| D <sub>4</sub> APTH  |               | .....C.....A.....A.....A.....T.....T.....T.....                       | 1330 |
| <b>MAJORITY</b>      |               |   |      |
| D <sub>4</sub> APTRQ |               | CCCACATGGAGGGCACGGGCTXCGGCTGGACCTGGCCCTACCTCCAGGCCCTXTCCTGGAGGTGGGGCA |      |
| D <sub>4</sub> APTR  |               | .....G.....G.....G.....C.....T.....T.....A.....G.....T.....           | 1394 |
| D <sub>4</sub> APTH  |               | .....GG.....C.....C.....C.....A.....C.....T.....C.....                | 1391 |
|                      |               | .....A.....A.....T.....T.....C.....T.....C.....                       | 1400 |

FIGURE 2 (cont'd)

|                        |  |      |
|------------------------|--|------|
| MAJORITY (SEQ ID NO:7) | GGAGATCGGGCCCTGGAGGACCTT   | 1464 |
| DNAPTAQ (SEQ ID NO:1)  | GG.....GG.....GG.....GG.....   | 1461 |
| DNAPTR (SEQ ID NO:2)   | G.....G.....AG.....G.....  | 1462 |
| DNAPTH (SEQ ID NO:3)   | .....T.....G.....  | 1463 |
| MAJORITY               | CAGCTGCAAGGCTGCTCTTGACCGACTXGGGCTTCGGCAAGACGGAGAAGACXGGCAAGC         |      |
| DNAPTAQ                | C.....A.....G.....A.....   | 1534 |
| DNAPTR                 | GC.....G.....G.....G.....  | 1531 |
| DNAPTH                 | TA.....T.....T.....G.....  | 1540 |
| MAJORITY               | GCTCCACCAAGGGGGCTGCTGAGGGCCCTXCGXGAGGGCCACCCATCGTGGAGAACATCCCTGCACTA |      |
| DNAPTAQ                | C.....C.....C.....C.....   | 1604 |
| DNAPTR                 | T.....G.....A.....G.....   | 1601 |
| DNAPTH                 | .....A.....G.....  | 1610 |
| MAJORITY               | CGGGGAAGCTCACCAAGCTAAAGAACACCTACATXGACCCCCCTGCCXGXCCTGCTCCACCCAGGGCC |      |
| DNAPTAQ                | T.....T.....G.....A.....   | 16   |
| DNAPTR                 | A.....A.....C.....C.....   | 16   |
| DNAPTH                 | .....G.....C.....AAG.....  | 168  |
| MAJORITY               | CGCCCTCCACACCCCTTCAACCACGGCCACGGCCAGGGCTTACTAGCTCCGACCCAAACCTGC      |      |
| DNAPTAQ                | .....A.....T.....  | 1744 |
| DNAPTR                 | .....TCC.....  | 1741 |
| DNAPTH                 | .....G.....G.....  | 1750 |

FIGURE 2 (cont'd)

FIGURE 2 (cont'd)

|   |          |
|---|----------|
| MAJORITY (SEQ ID NO:7) AGCTTCCCCAAGGTGGGATTGACAAGACCC <del>TGGAGGAGGCCGGGTACCTGGAGA</del> | 2164     |
| DNADTAO (SEQ ID NO:1) .....   | DNADTAO  |
| DNADTR (SEQ ID NO:2) .....  | DNADTR   |
| DNADTH (SEQ ID NO:3) .....  | DNADTH   |
| MAJORITY .....  | MAJORITY |
| DNADTAO .....   | DNADTAO  |
| DNADTR .....  | DNADTR   |
| DNADTH .....  | DNADTH   |
| MAJORITY .....  | MAJORITY |
| DNADTAO .....   | DNADTAO  |
| DNADTR .....  | DNADTR   |
| DNADTH .....  | DNADTH   |
| MAJORITY .....  | MAJORITY |
| DNADTAO .....   | DNADTAO  |
| DNADTR .....  | DNADTR   |
| DNADTH .....  | DNADTH   |
| MAJORITY .....  | MAJORITY |
| DNADTAO .....   | DNADTAO  |
| DNADTR .....  | DNADTR   |
| DNADTH .....  | DNADTH   |

23  
2304  
2301  
2310  
231  
230  
2300  
2380  
2444  
2441  
2450

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正四面體

FIGURE 2 (cont'd)

| MAJORITY (SEQ ID NO:7) | CCCCCTGGAGGTGGAGGTGGGATGGGGAGCTGGCTCTCCCAAGGAGTAG |
|------------------------|---|
| DNAPTAQ (SEQ ID NO:1)  | .....A.....                                       |
| DNAPTR (SEQ ID NO:2)   | .....CC.....                                      |
| DNAPTH (SEQ ID NO:3)   | .....T.....                                       |

正義のための政治

FIGURE 3

五言律詩二首

FIGURE 3 (cont'd)

|                        |  |                             |
|------------------------|--|-----------------------------|
| MAJORITY (SEQ ID NO:8) | RGLLAKDVLAVLALRECLDLXPGDDOPMHLAYLLDPSNTTPEGUARRYGGEWTE                         | DAGERALLSERLFXNLXX          |
| TAQ PRO (SEQ ID NO:4)  | S.....S.....G.....P.....   | E.....A.....A.....A.....W.G |
| TR PRO (SEQ ID NO:5)   | I.....F.....E.....   | F.....A.....QT.....KE       |
| TTH PRO (SEQ ID NO:6)  | S.....V.....   | A.H.....HR.....LK.....420   |
| MAJORITY               | RLEGEERILLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAAEIRRRLFEVVFRLAGHPFNLNSRD       |                             |
| TAQ PRO                | R.....R.....A.....R.....   | R.....A.....A.....A.....    |
| TR PRO                 | K.....E.....R.....   | EA.....V.....Q.....         |
| TTH PRO                | K.....H.....   | L.....                      |
| MAJORITY               | QLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKNTYIDPLPXLVHPRIG         |                             |
| TAQ PRO                | .....  | S.....                      |
| TR PRO                 | .....  | D.R.....                    |
| TTH PRO                | R.....L....O.....  | H.....V.....S.....          |
| MAJORITY               | RLHTRFNQATATGRLSSSDPHLQNI PVRTPLQORI RRAFVAEEGWWXVALDYSQI ELRVL AHL SGDEHL     |                             |
| TAQ PRO                | .....  | I.....L.....                |
| TR PRO                 | .....  | V.....V.....                |
| TTH PRO                | .....  | A.....A.....                |
| MAJORITY               | IRVFQEGRDI HTQTASYMFF GVPPEAVDPLMRRAAKTI INFQVLYGMSAHL SQEELAI PYEEAVAFI ERYFO |                             |
| TAQ PRO                | E.....   | R.....Q.....                |
| TR PRO                 | .....  | S.....G.....                |
| TTH PRO                | .....  | G.....V.....                |

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FIGURE 3 (cont'd)

|                        |   |               |               |
|------------------------|---|---------------|---------------|
| MAJORITY (SEQ ID NO:8) | S P P K V U R A W I E K T L I E G G R R R G Y V E T L F G R R R Y V P D L H A R V K S V R E A E R M A F F H M P V O Q T A A D L M K K L A M V K L |               |               |
| TAQ PRO                | (SEQ ID NO:4)   | Y . . . . .   | E . . . . .   |
| TRI PRO                | (SEQ ID NO:5)   | G . . . . .   | G . . . . .   |
| THI PRO                | ( SEQ ID NO:6)  | K . . . . .   | R . . . . .   |
| MAJORITY               | F P R I X E M G A R M L Q V H D E L V L E A P K X R A E X V A A L A K E V M E G V Y P L A V P L E V V G X G E D W L S A K E X                     |               |               |
| TAQ PRO                |   | E . . . . .   | E . . . . .   |
| TRI PRO                |   | Q . L . . . . | D . R . . . . |
| THI PRO                |   | R . . . . .   | W . Q . . . . |
|                        |   | L . . . . .   | L . . . . .   |
|                        |   | Q A . . . . . | A . . . . .   |
|                        |   | E . . . . .   | K A . . . . . |
|                        |   |               | M . . . . .   |
|                        |   |               | G . . . . .   |

FIGURE 4

Genes for Wild-Type and Pol(-) DNAPTAq

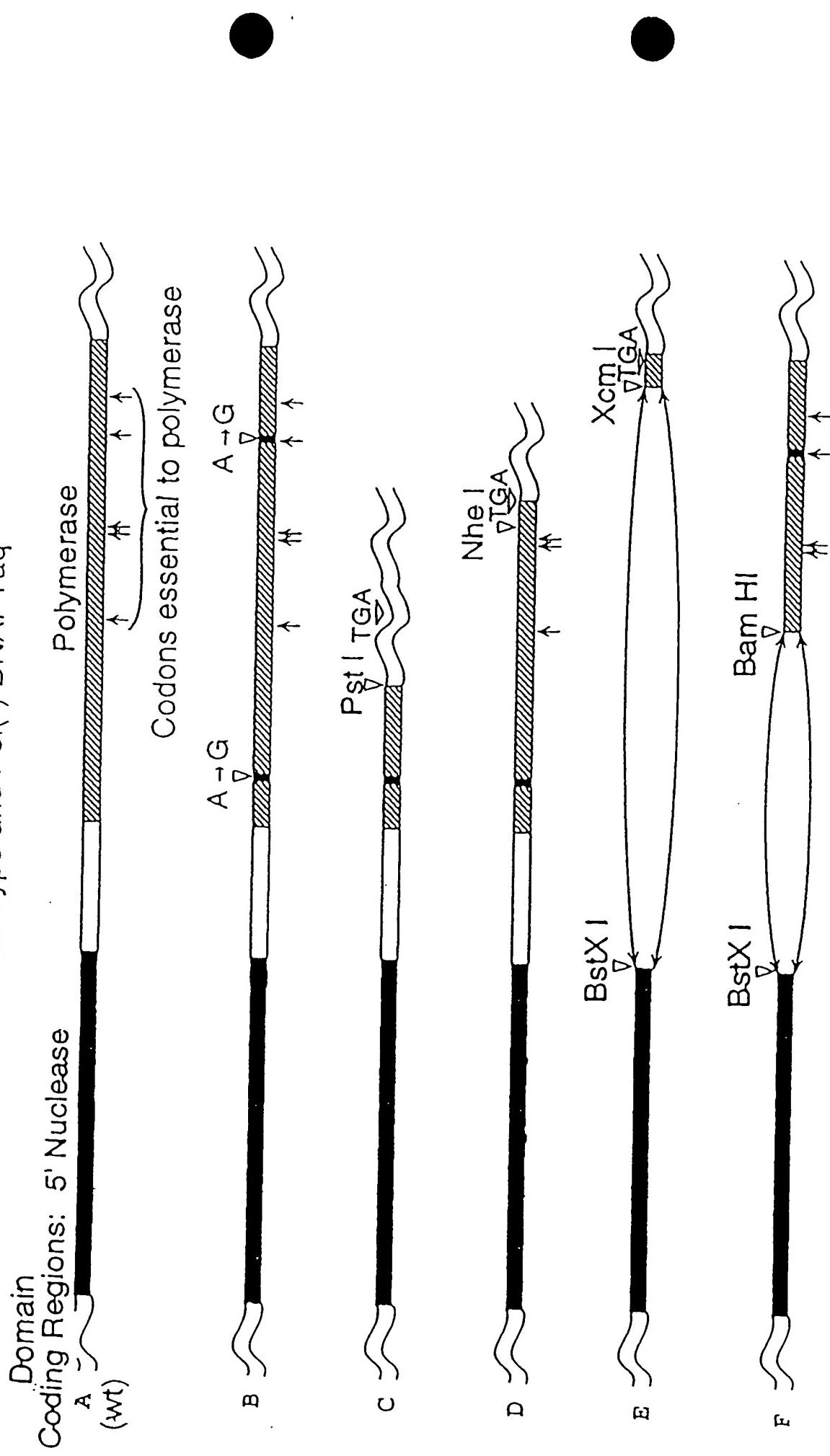


FIGURE 5

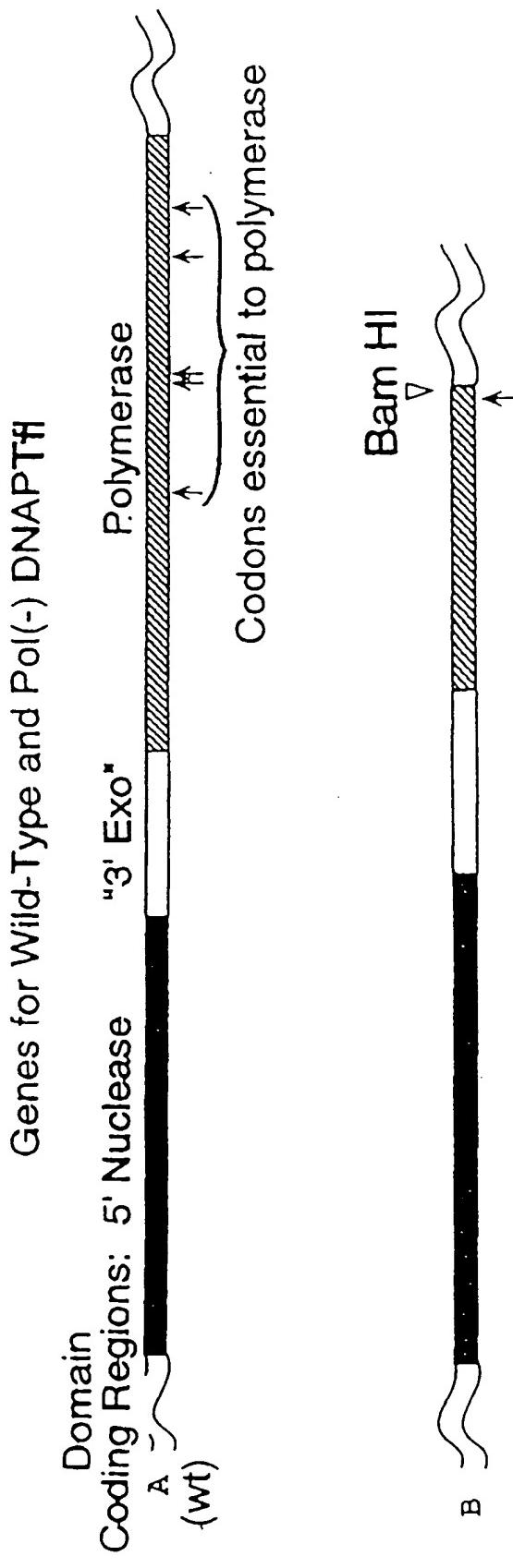


FIGURE 6

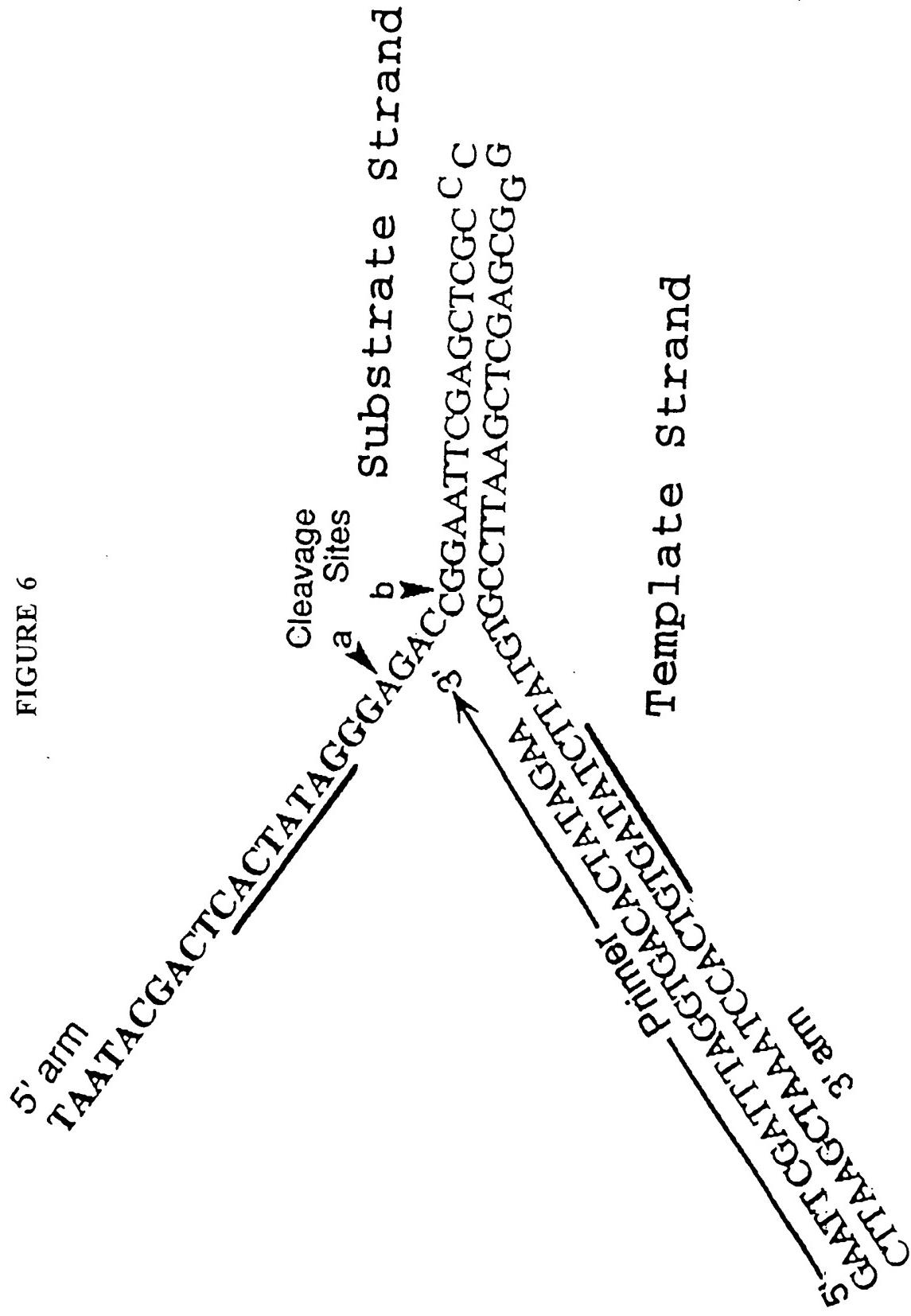
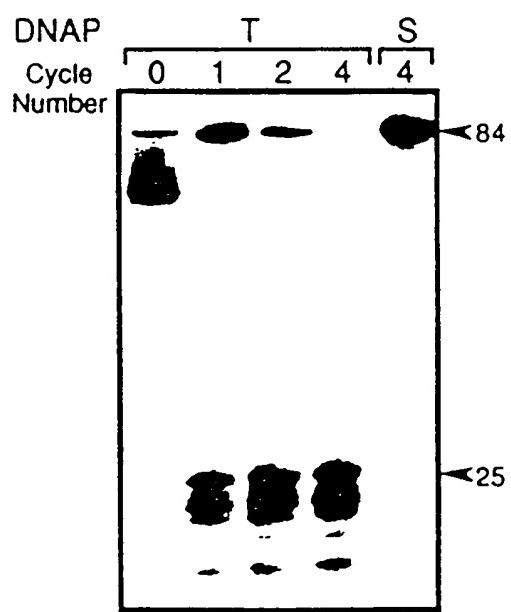


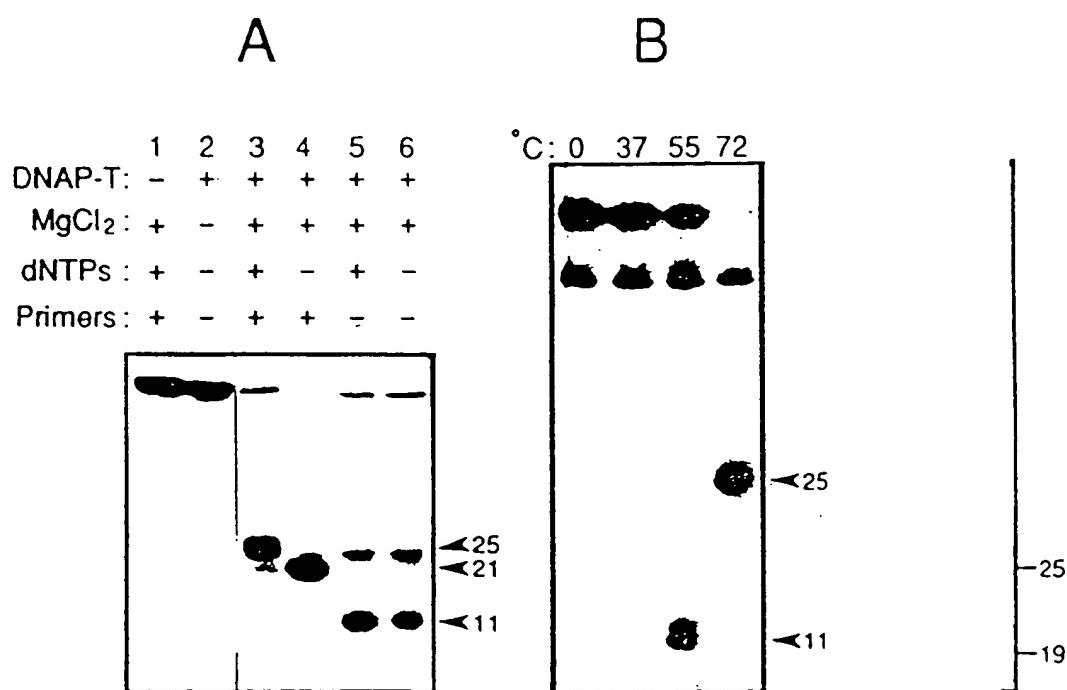
FIGURE 7



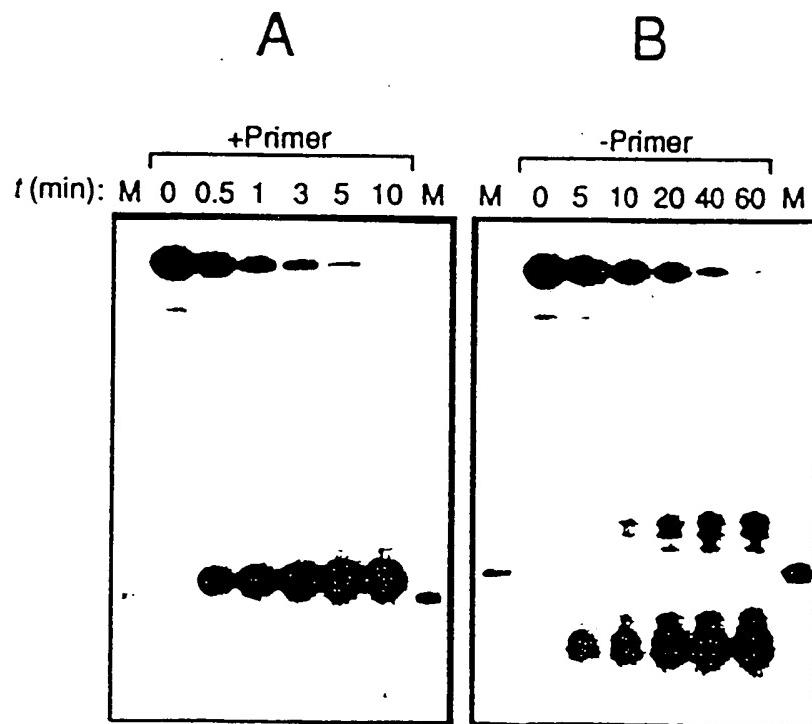
1007428 021202

FIGURE 8



**FIGURE 9**

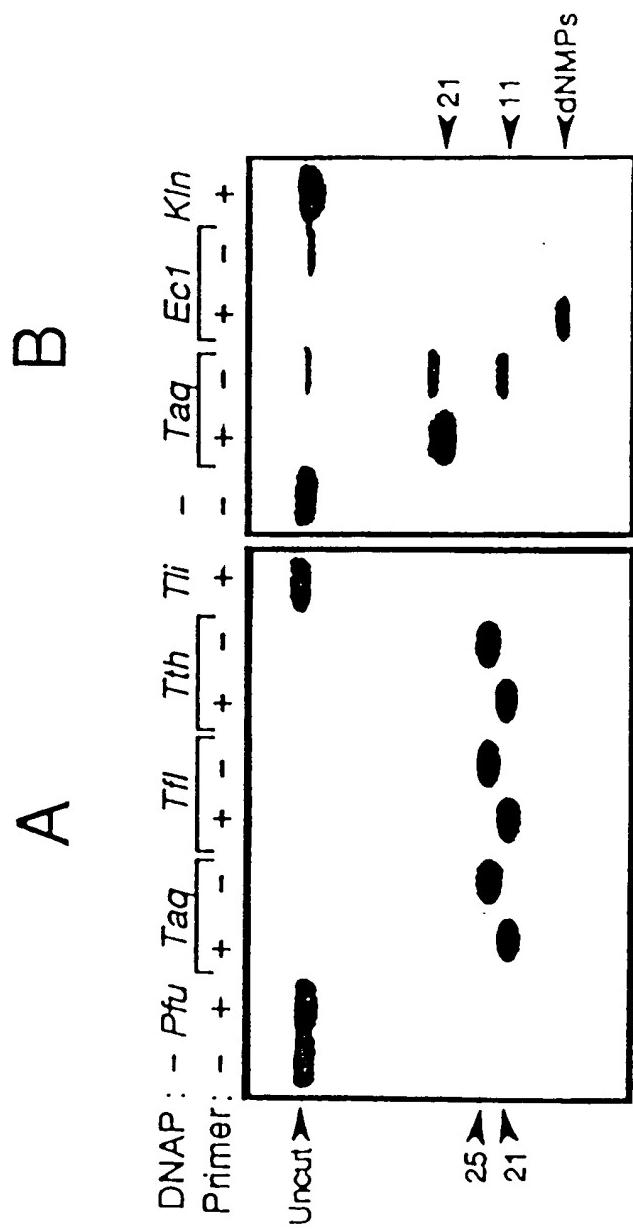
**FIGURE 10**



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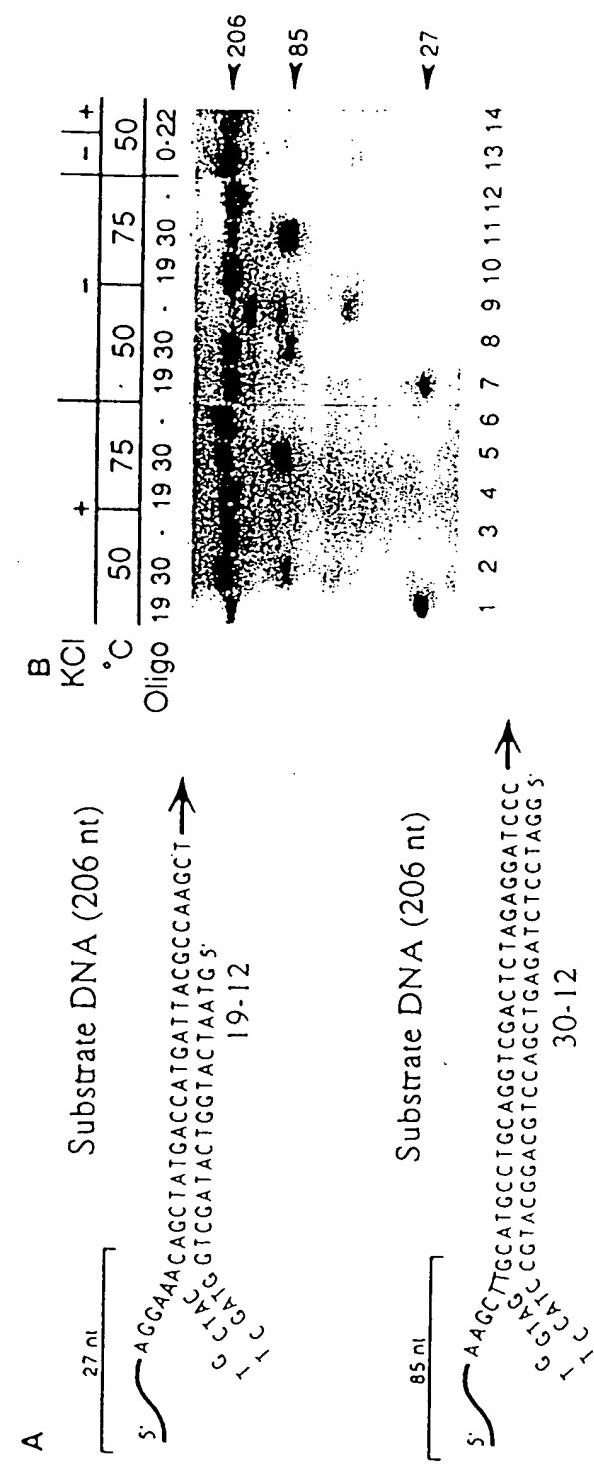
卷之三

FIGURE 11



202720 " 32E4L00T

FIGURE 12



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FIGURE 13

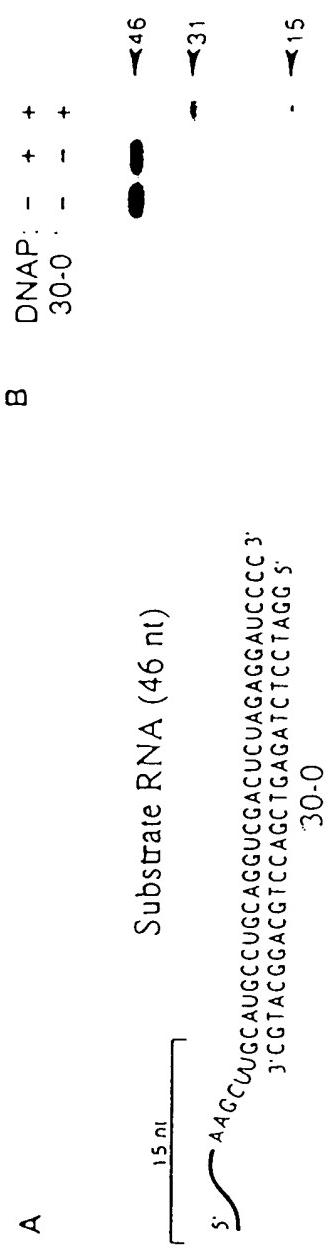
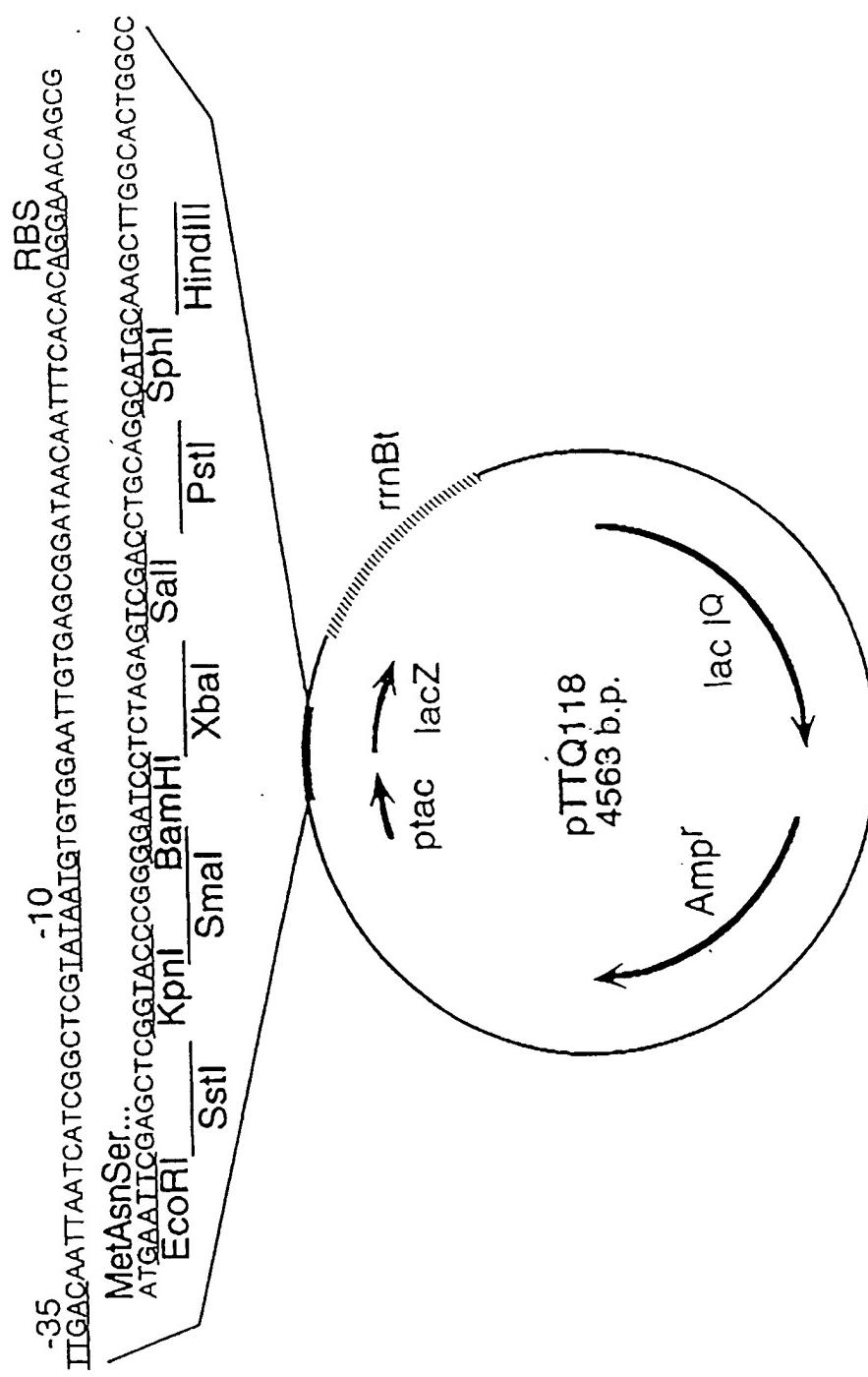


FIGURE 14



RBS: Ribosome binding site

ptac: Synthetic tac promoter

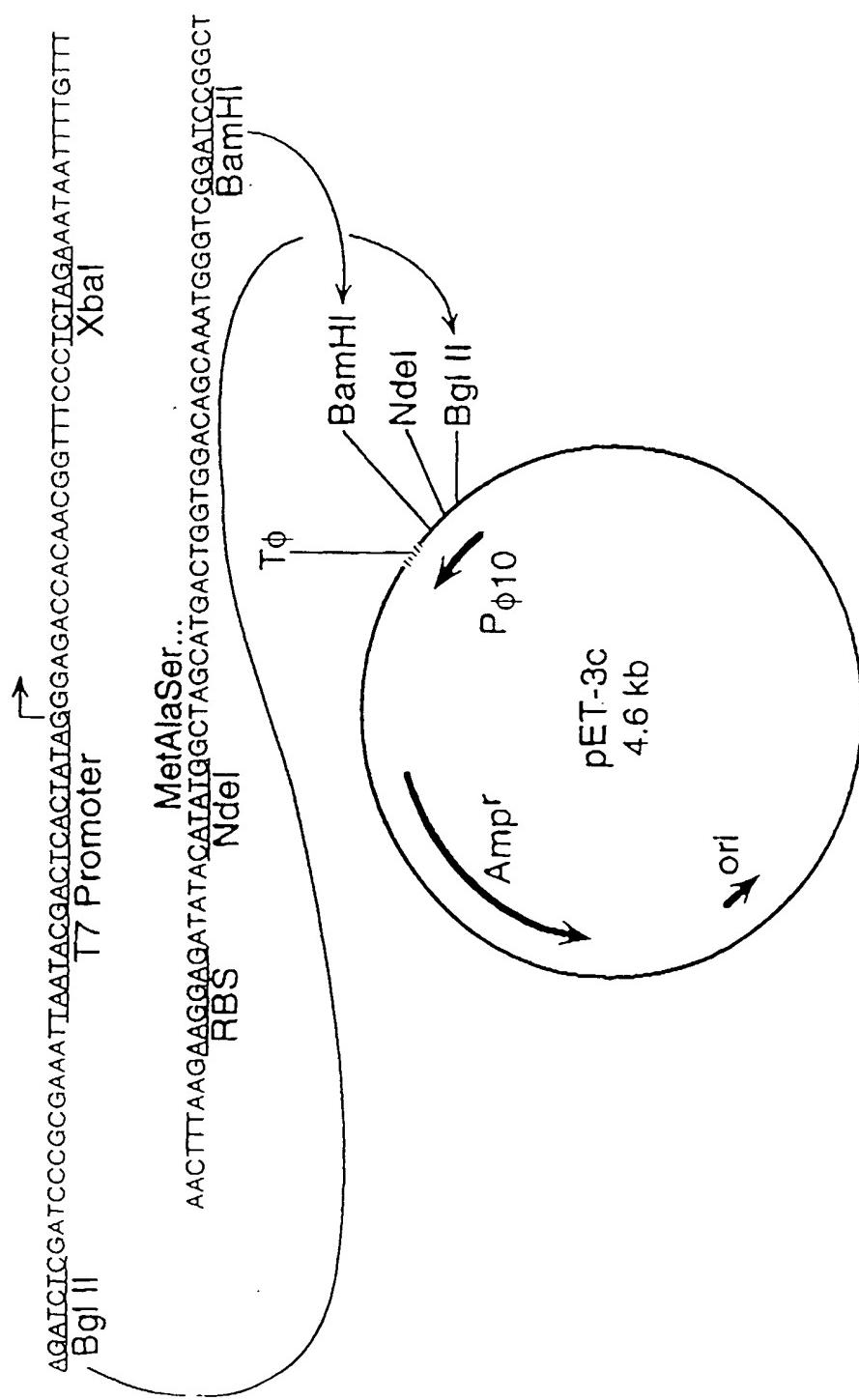
lacIQ: Lac repressor gene

lacZ: Beta-galactosidase alpha fragment

rrnBt: E. coli rrnB transcription terminator

2021-20 "Bacteriophage

FIGURE 15



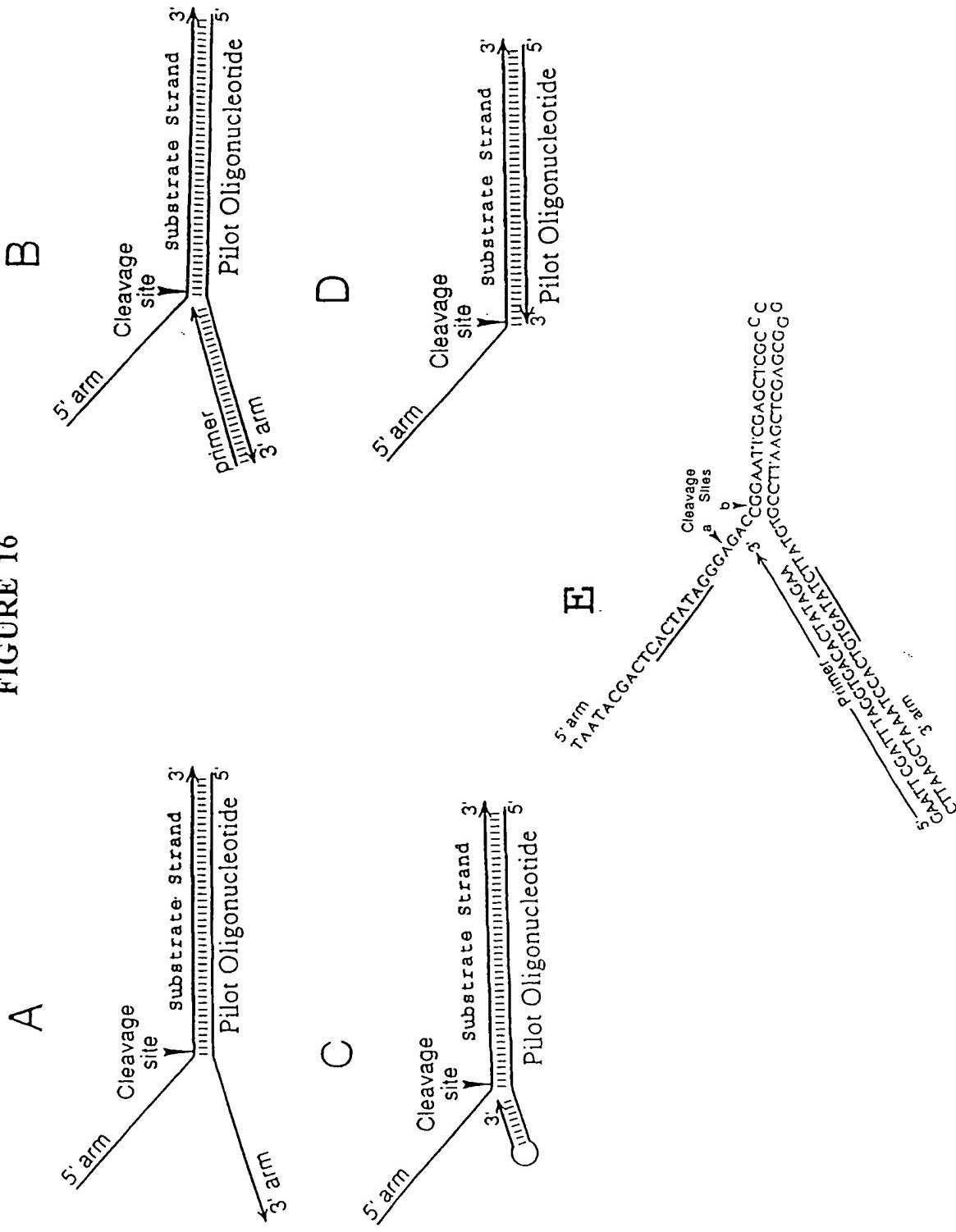
P<sub>Φ</sub>10: Bacteriophage T7  $\phi$ 10 promoter

T<sub>Φ</sub>: T7  $\phi$  Terminator

RBS: Ribosome binding site

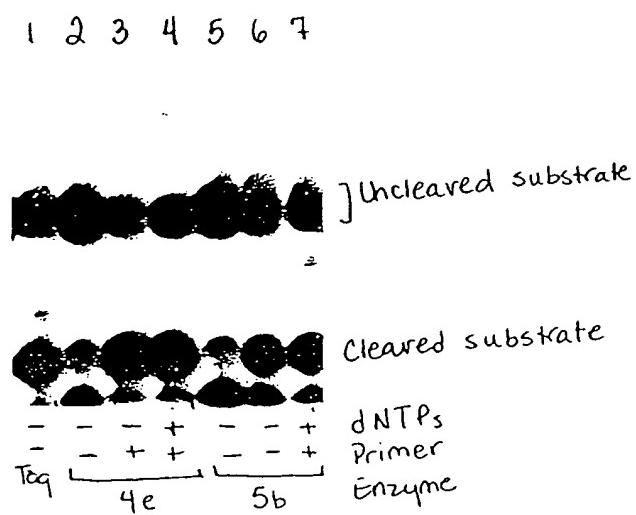
25

FIGURE 16



400074328 021202

FIGURE 17



2020 " 2020 " 2020 " 2020 "

FIGURE 18

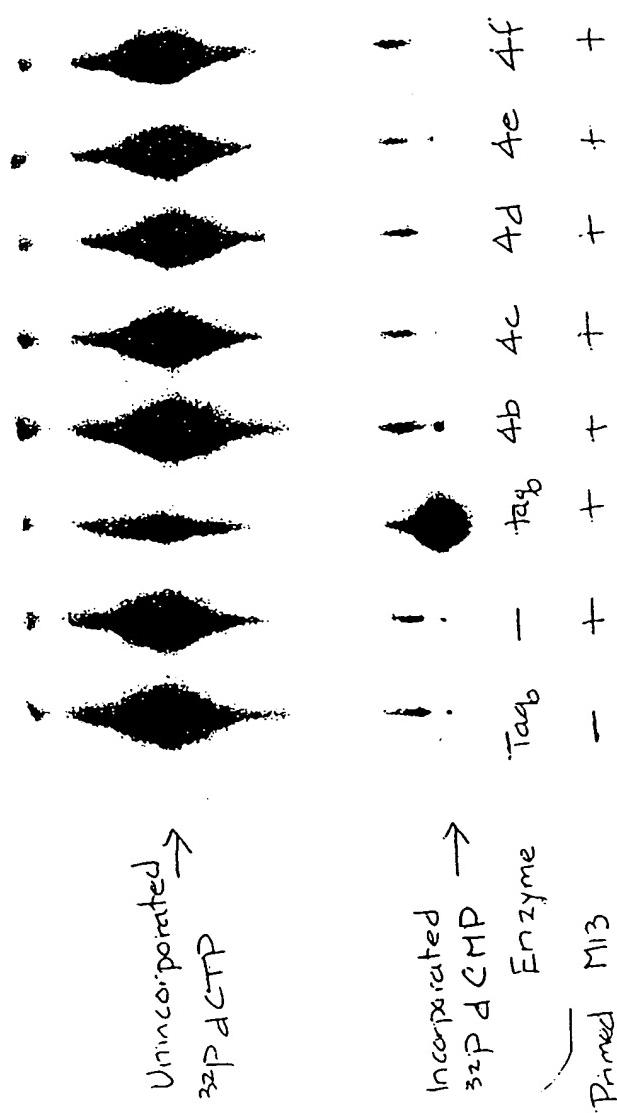
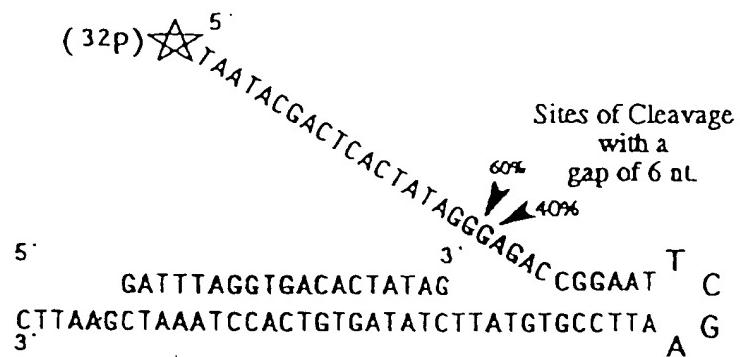


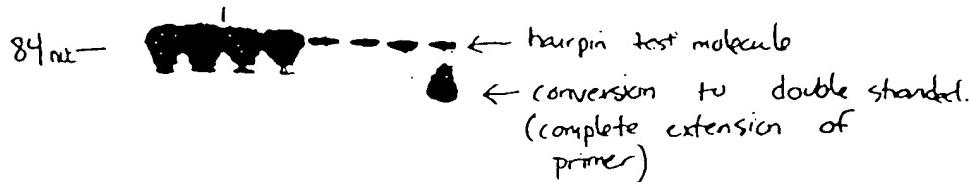
FIGURE 19

A



B

|     |                     | "4d"             |                  | "Ab"               |       |  |  |
|-----|---------------------|------------------|------------------|--------------------|-------|--|--|
|     |                     | (2 pr. mutation) |                  | Unmodified         |       |  |  |
| No. | Polymerase Activity | small            |                  | DNATP Tag          |       |  |  |
|     |                     | 5                | 6                | 7                  | 8     |  |  |
| 1   | C <sup>de</sup> +   | T <sup>d</sup> + | T <sup>d</sup> - | T <sup>d</sup> / + | - NTP |  |  |
| 2   |                     |                  |                  |                    |       |  |  |
| 3   |                     |                  |                  |                    |       |  |  |
| 4   |                     |                  |                  |                    |       |  |  |



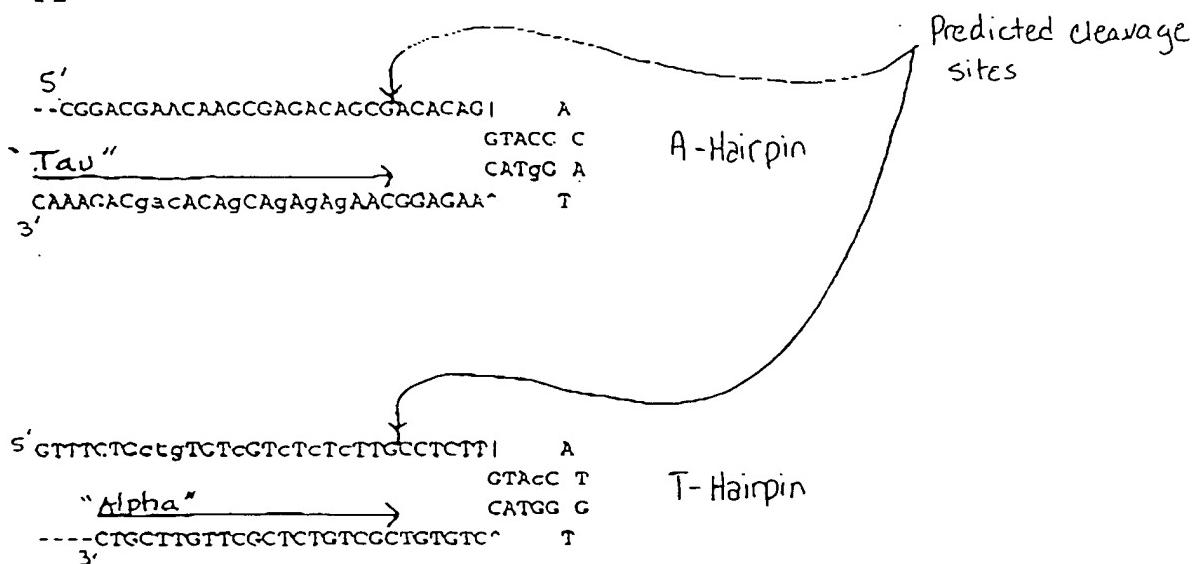
desired product →      } Multiple bands  
2 nuc.                  } caused by polymerization

↑ some aberrant cleavage with  
"4b" because of residual  
polymerase activity.

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FIGURE 20

A

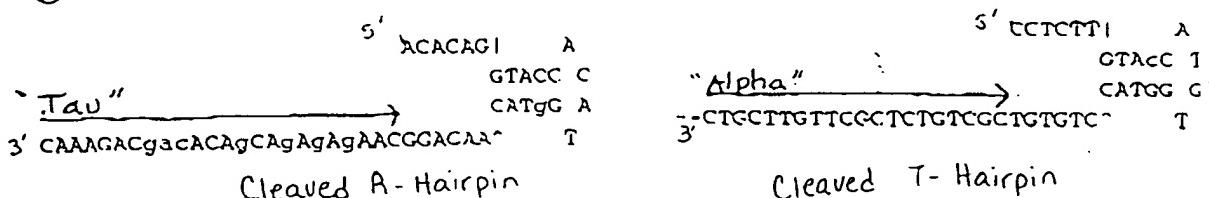


B

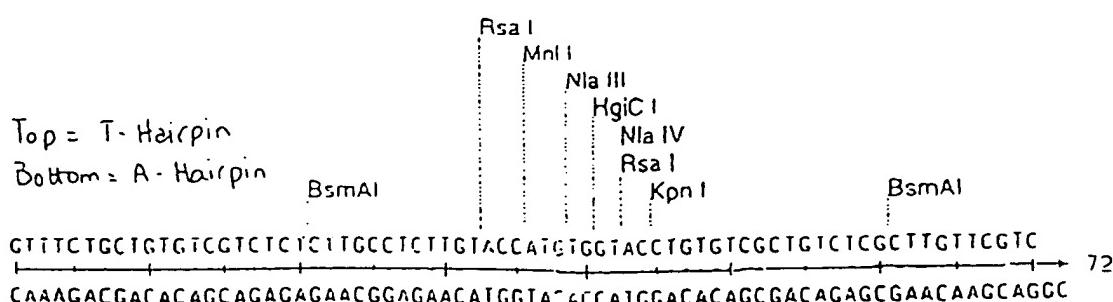
Sequence of alpha primer:

5' GAC GAA CAA CGG AGA CAG CG 3'

C

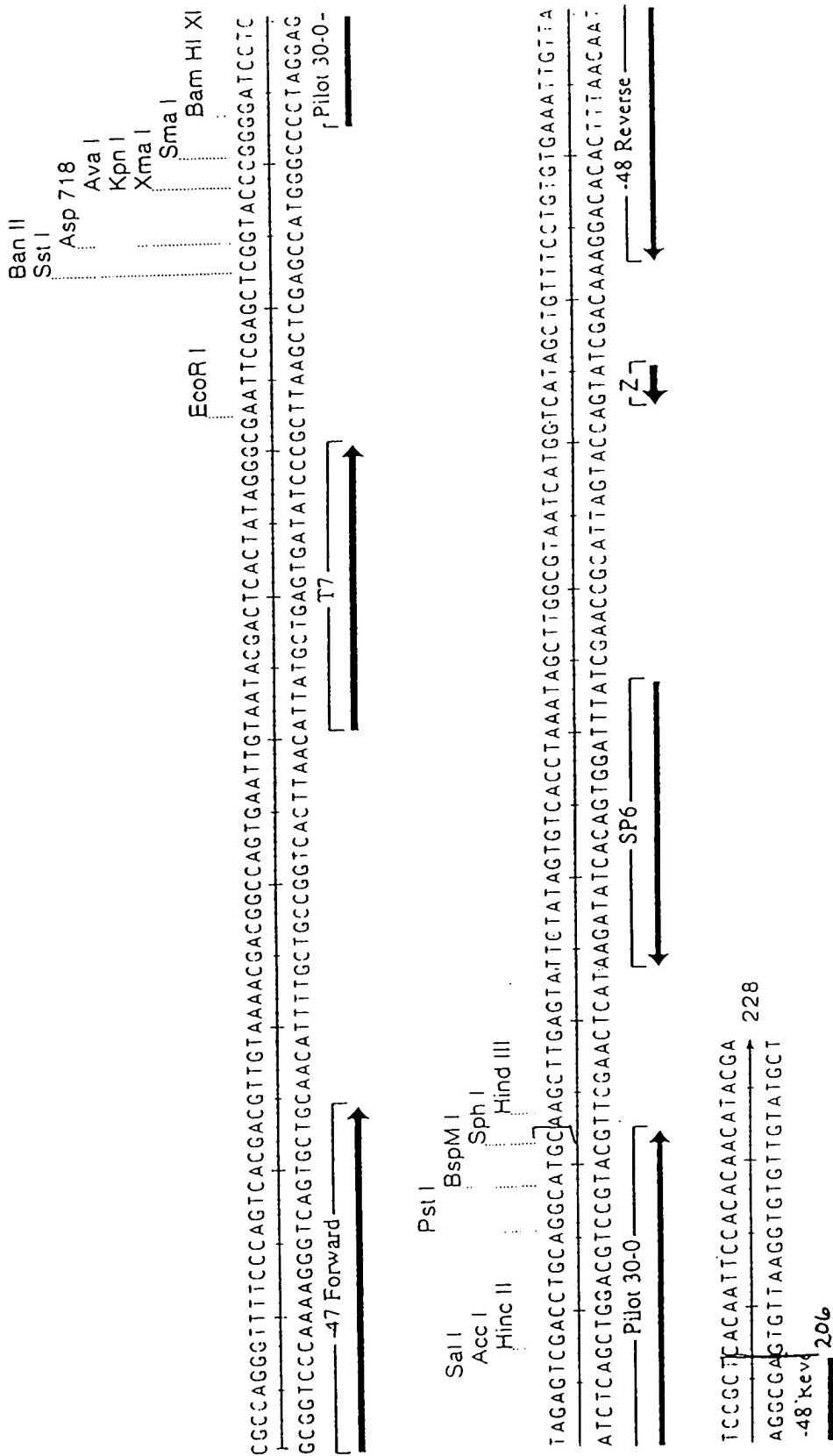


D



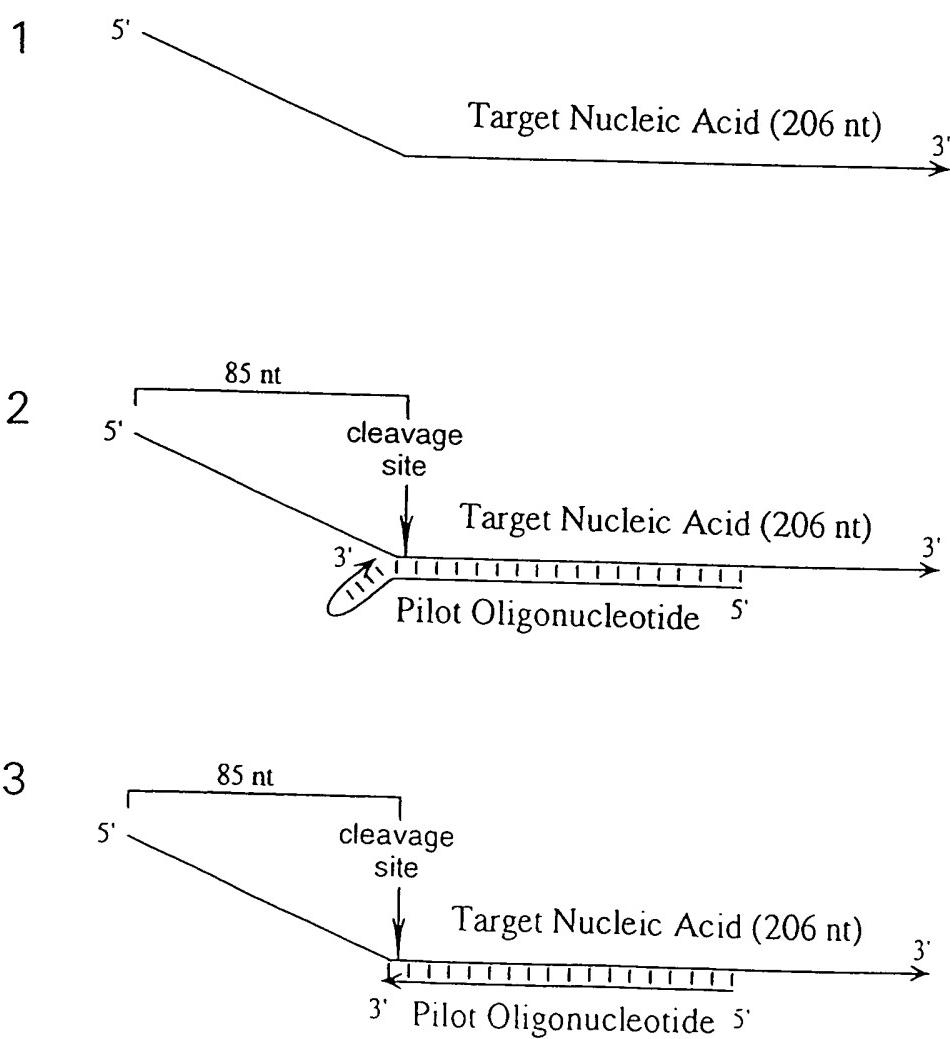
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FIGURE 21



**FIGURE 22A**

40024338 " 021202



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FIGURE 22B

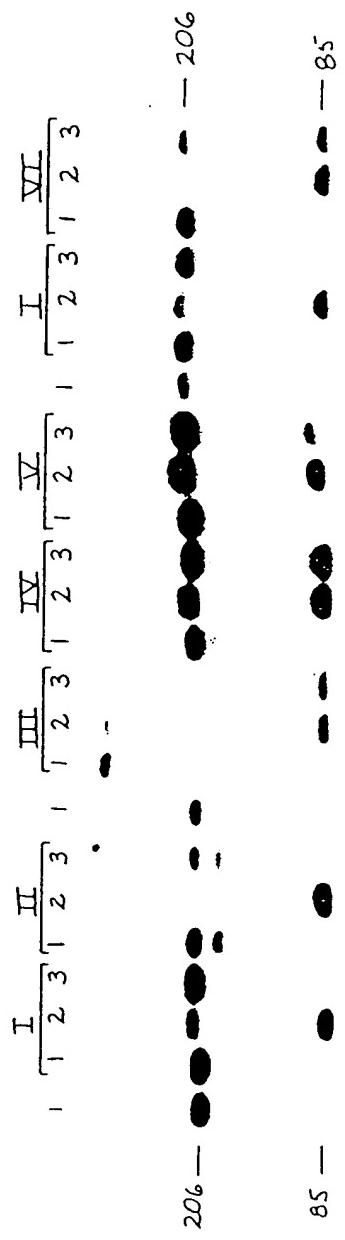
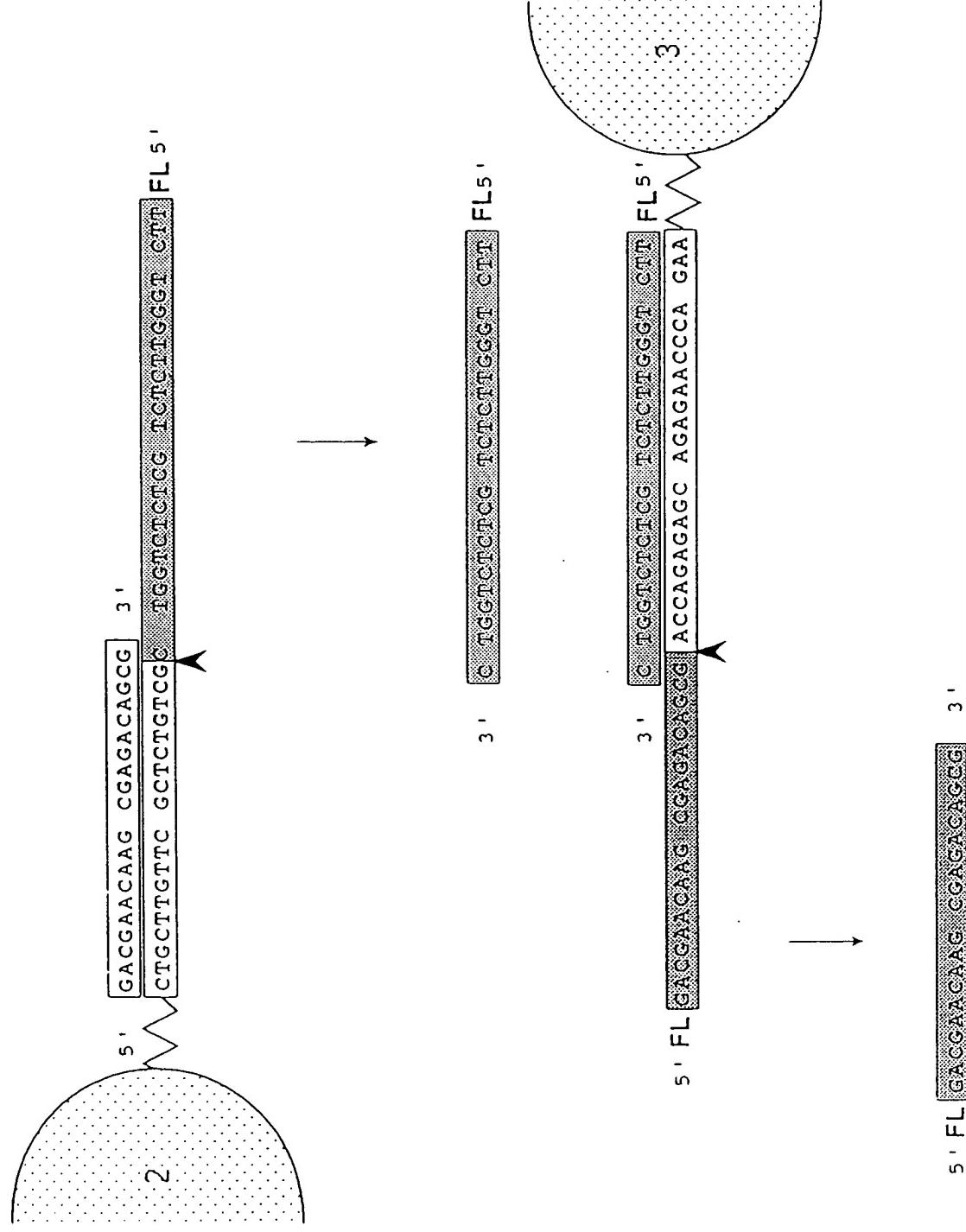
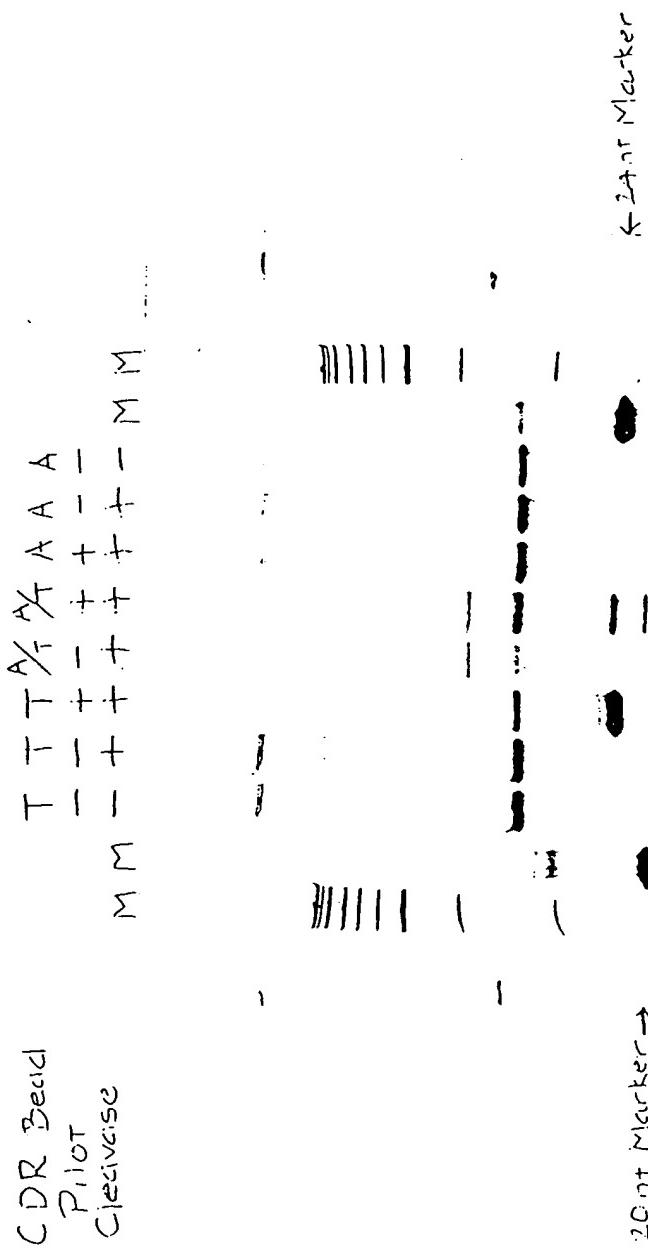


FIGURE 23

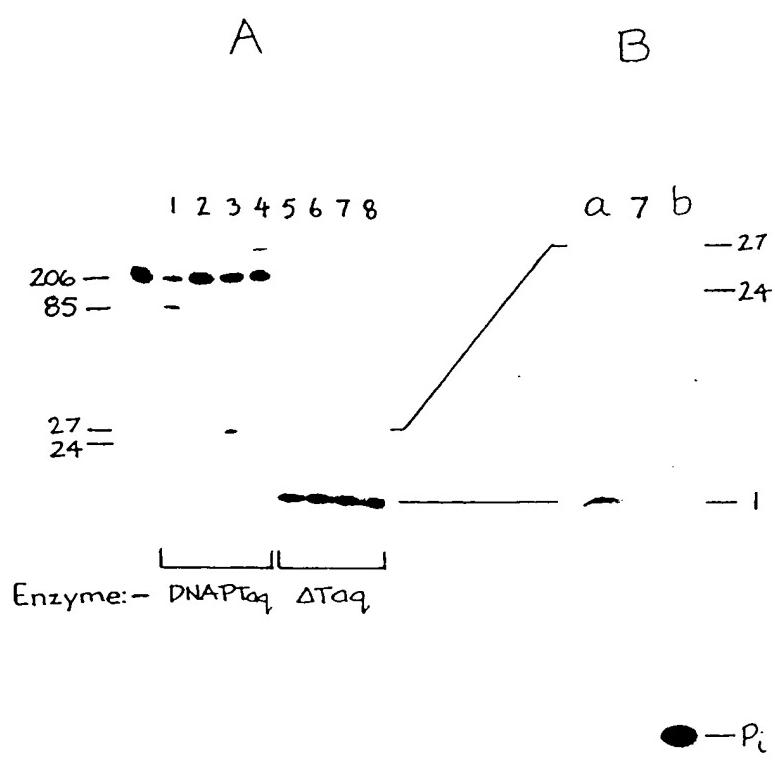


2020-07-22 "22541200T

FIGURE 24



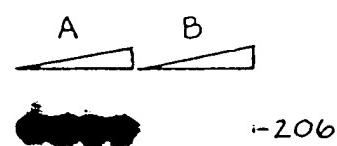
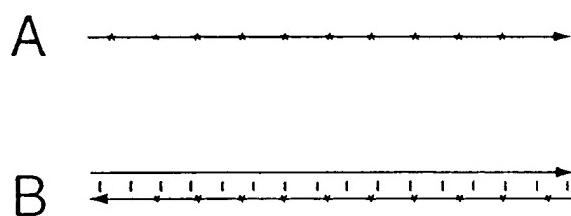
## FIGURE 25



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400743228 - 0641202

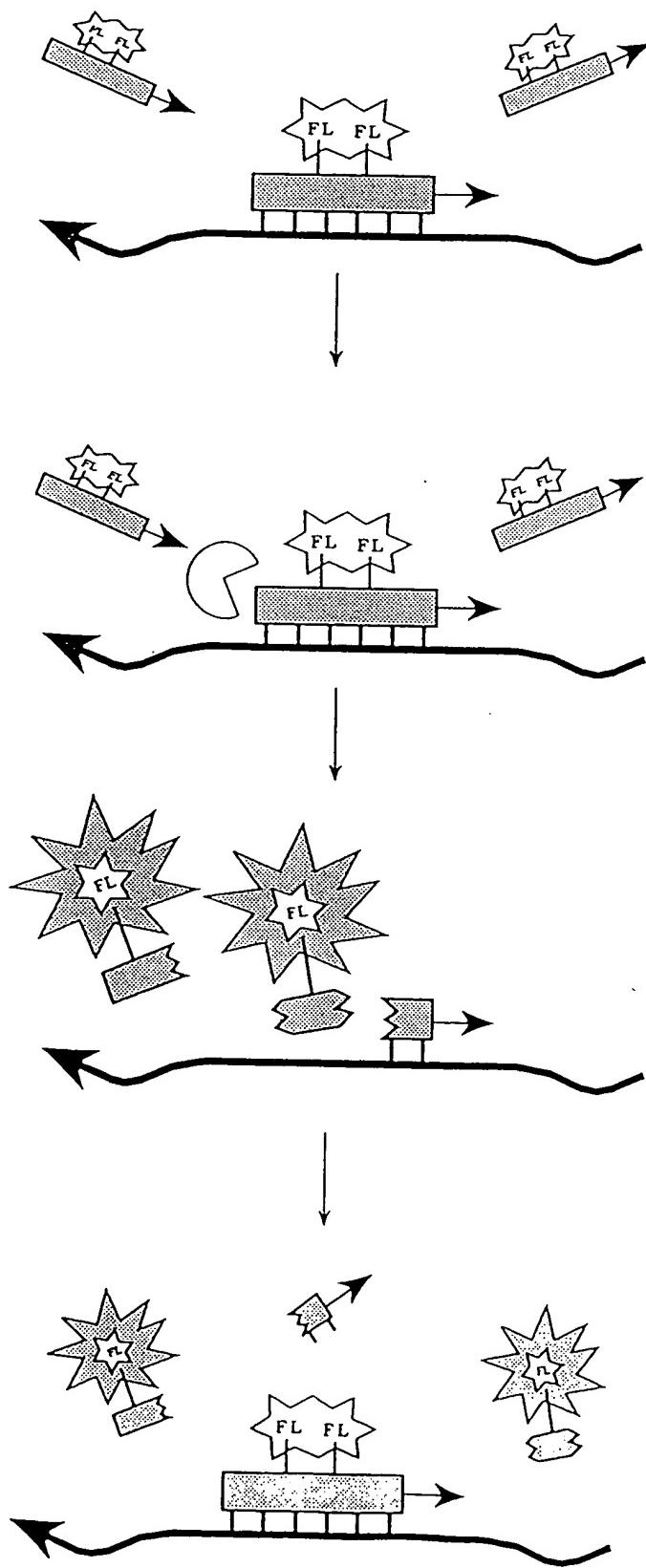
FIGURE 26



$$\star = ^{32}\text{P}$$

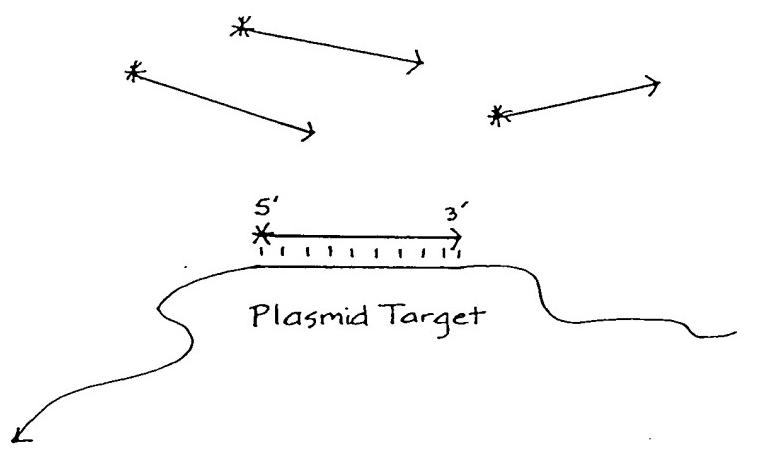
100243226 "021202

FIGURE 27



100% 32P "DNA" 2002

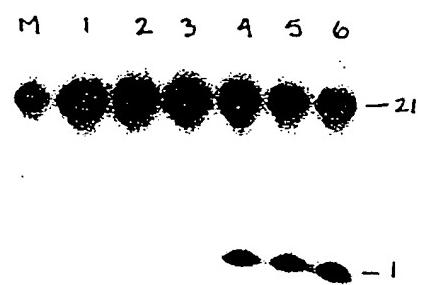
FIGURE 28A



\* =  $^{32}\text{P}$  5' terminal phosphate

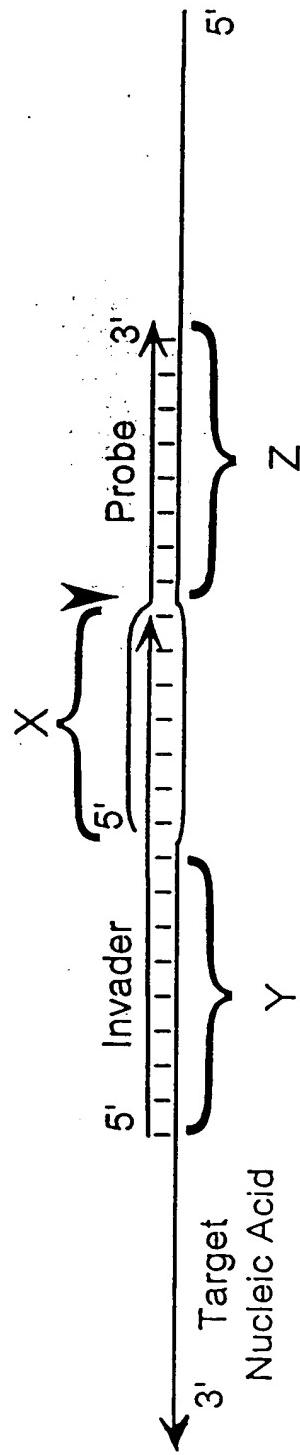
10074326 021202

**FIGURE 28B**



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FIGURE 29



**FIGURE 30**

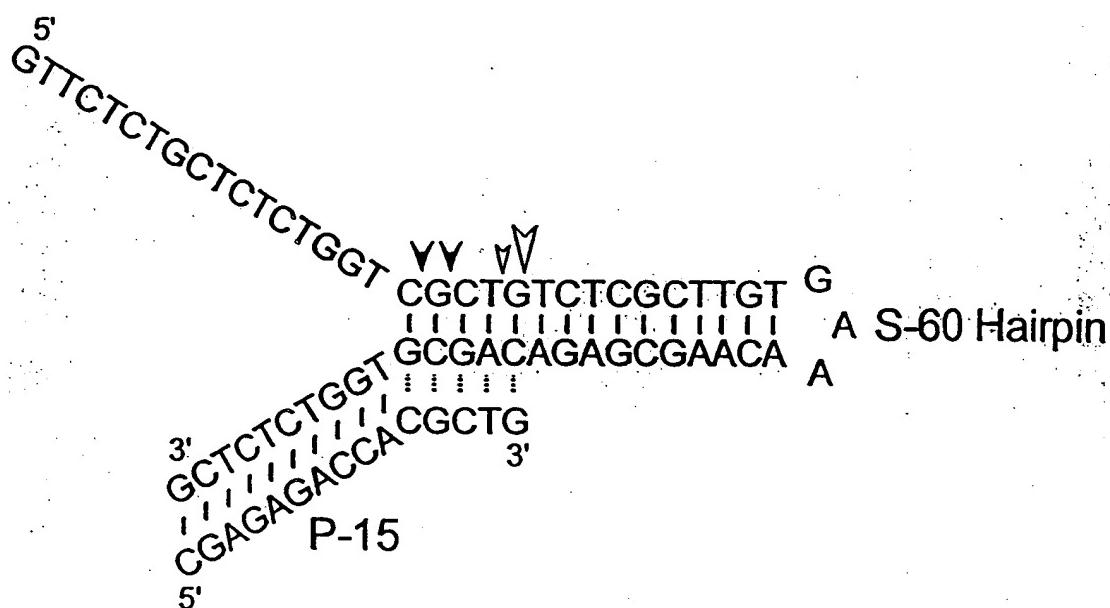
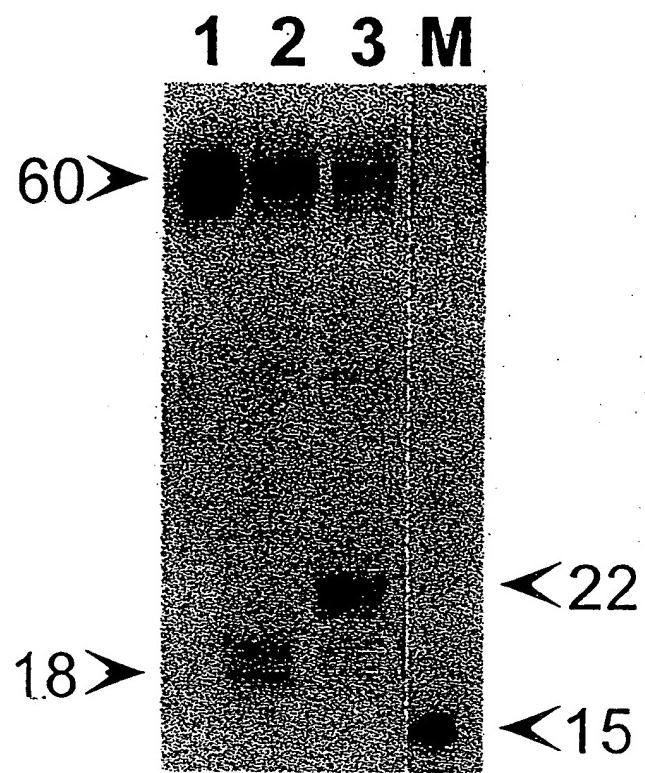


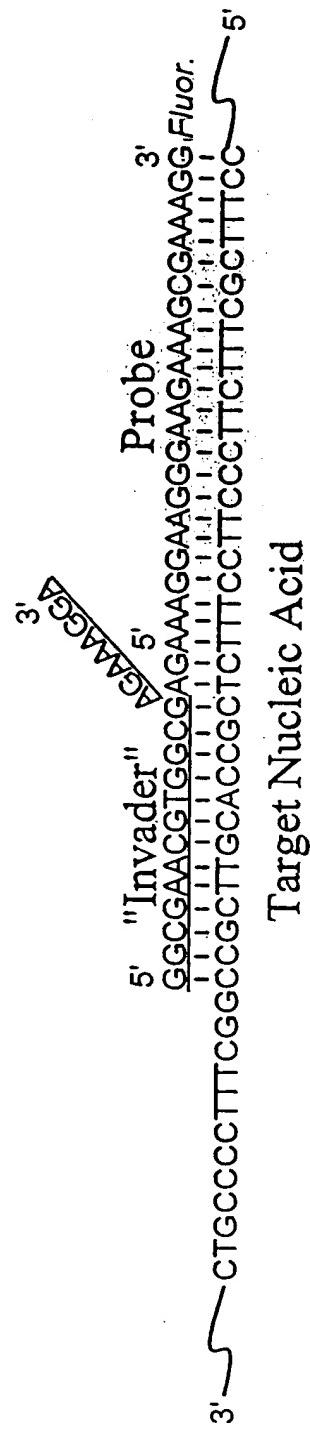
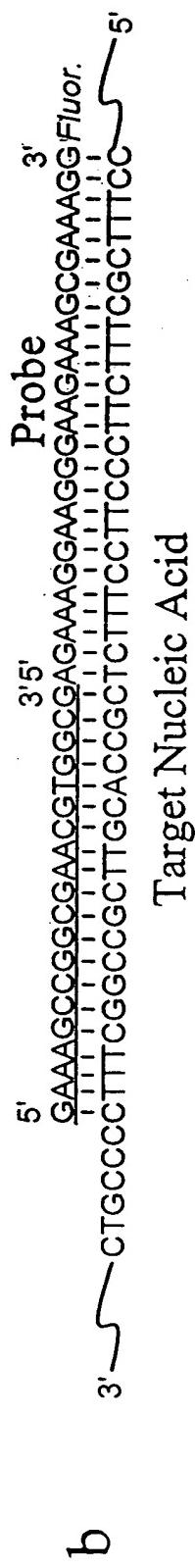
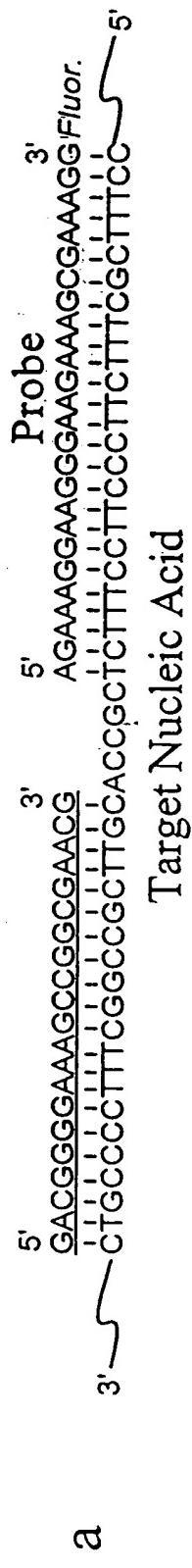
FIGURE 31



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**FIGURE 32**



44

1 2 3 4 5 6 7 8

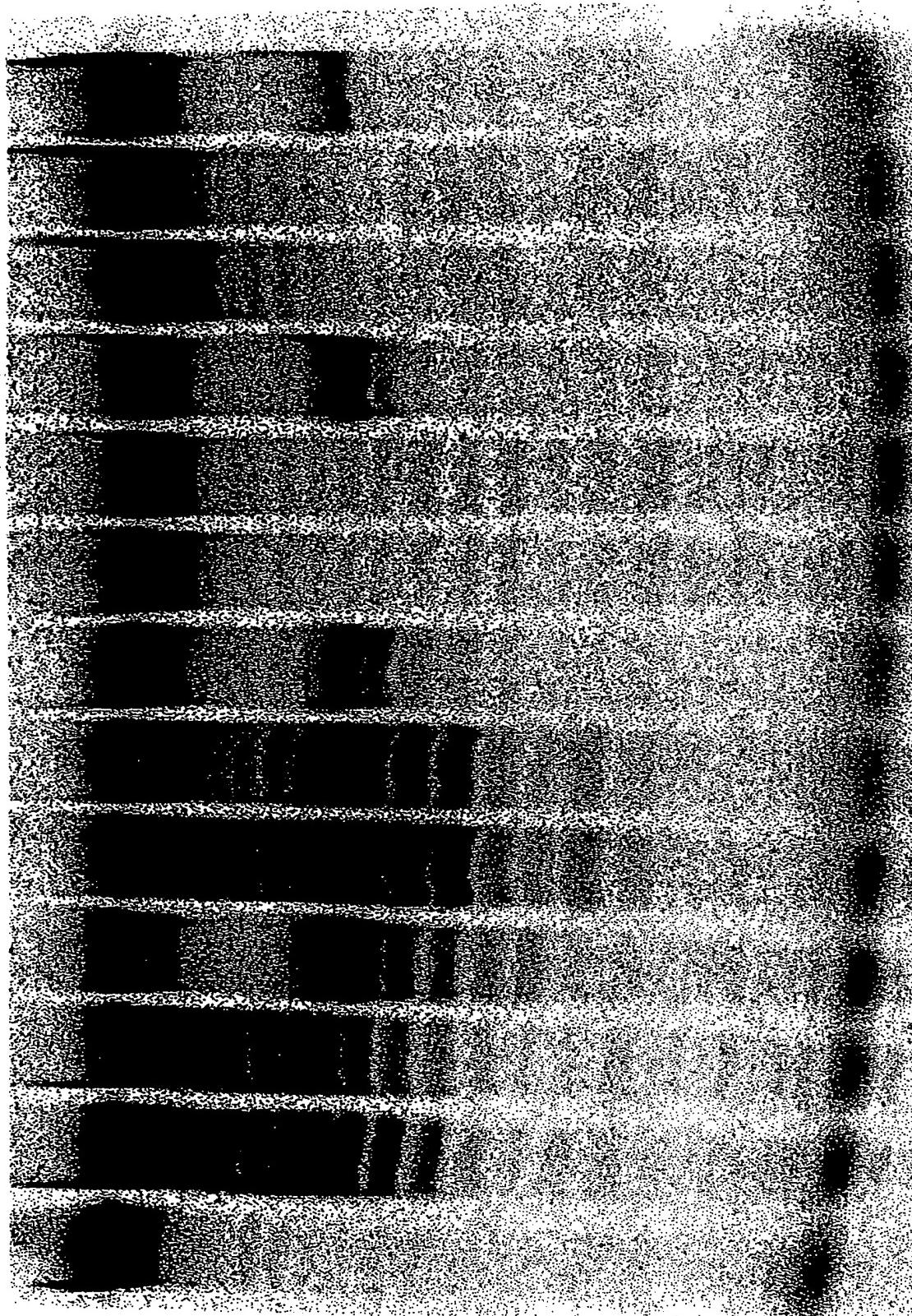
26>

45

FIGURE 34

202 F 20" 82E+1200T

M 1 2 3 4 5 6 7 8 9 10 11 12



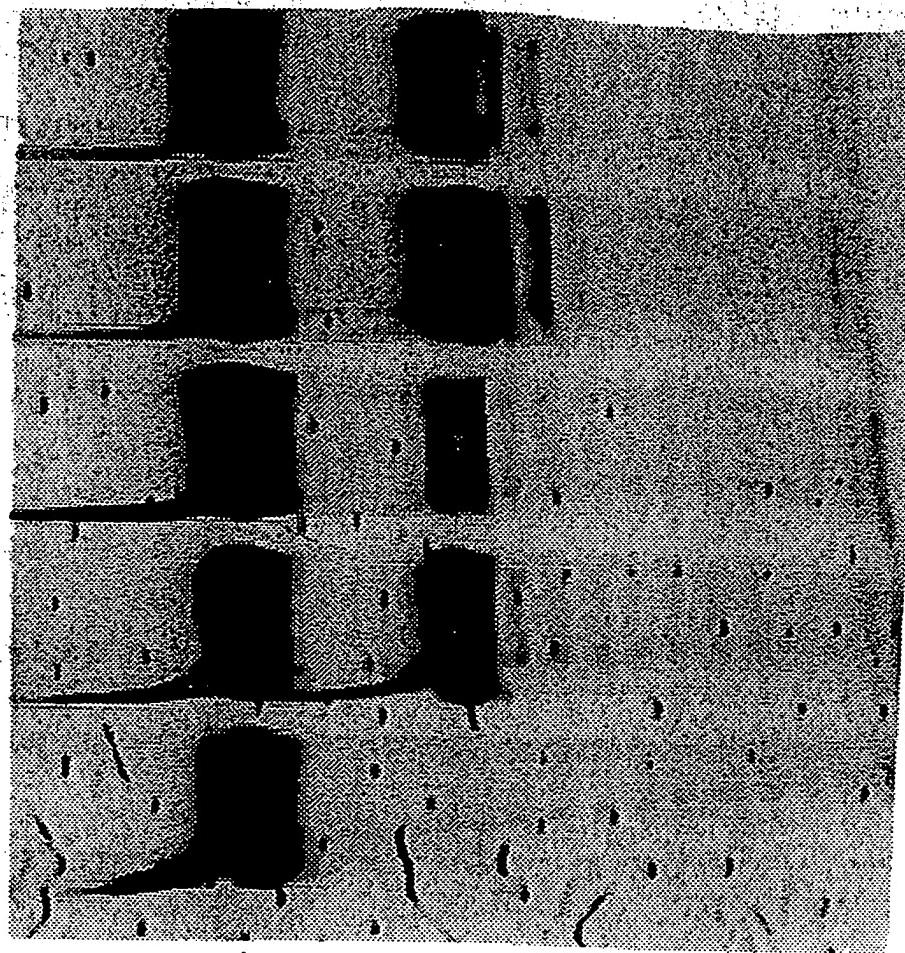
26 ➤

46

FIGURE 35

2021" 82E1200T

1 2 3 4 5



26 →

47

FIGURE 36  
ELECTROPHORESIS

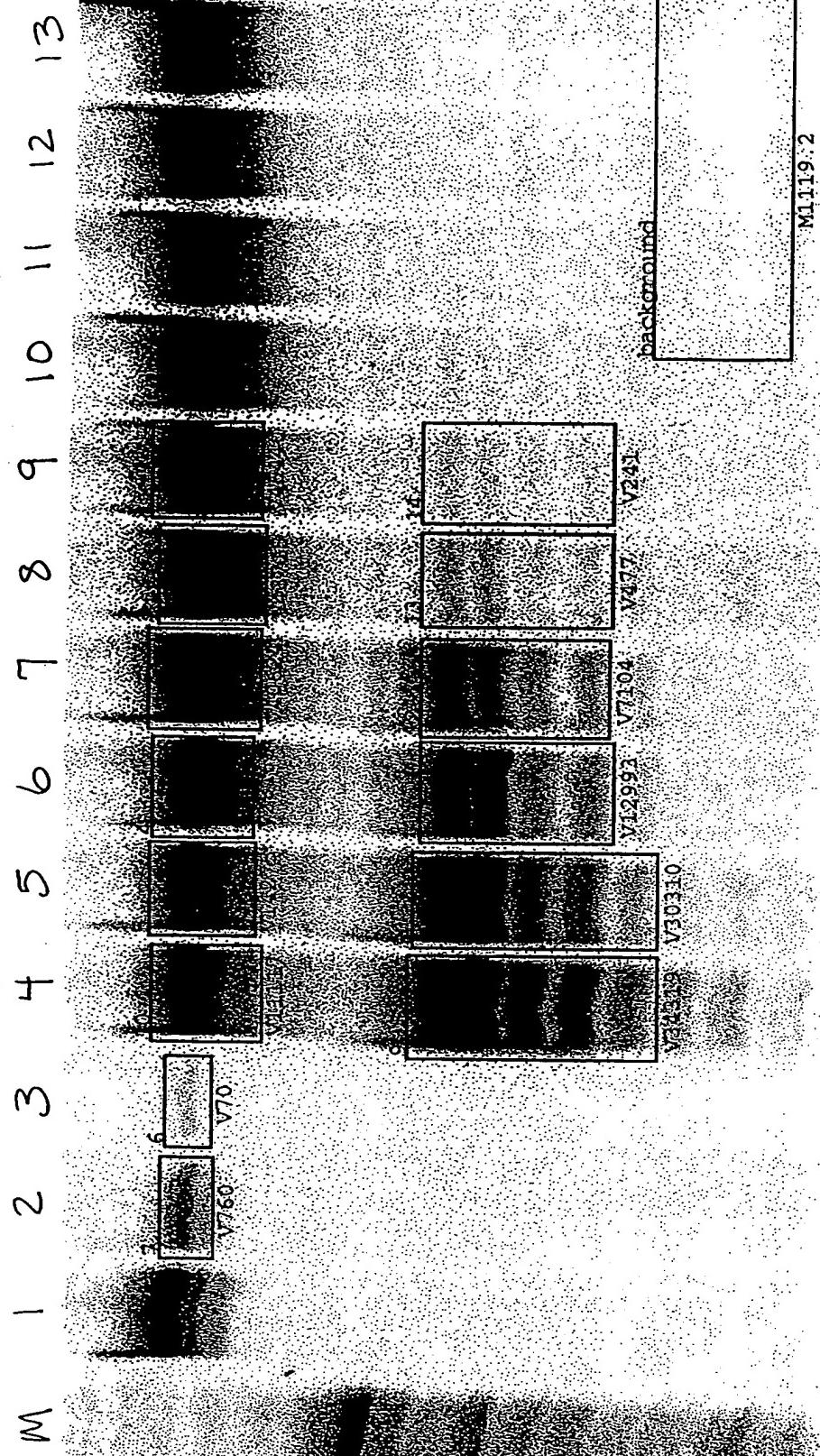


FIGURE 37

202120" 22E42°00'W

1 2 3 4 5 6 7 8 9 10 11

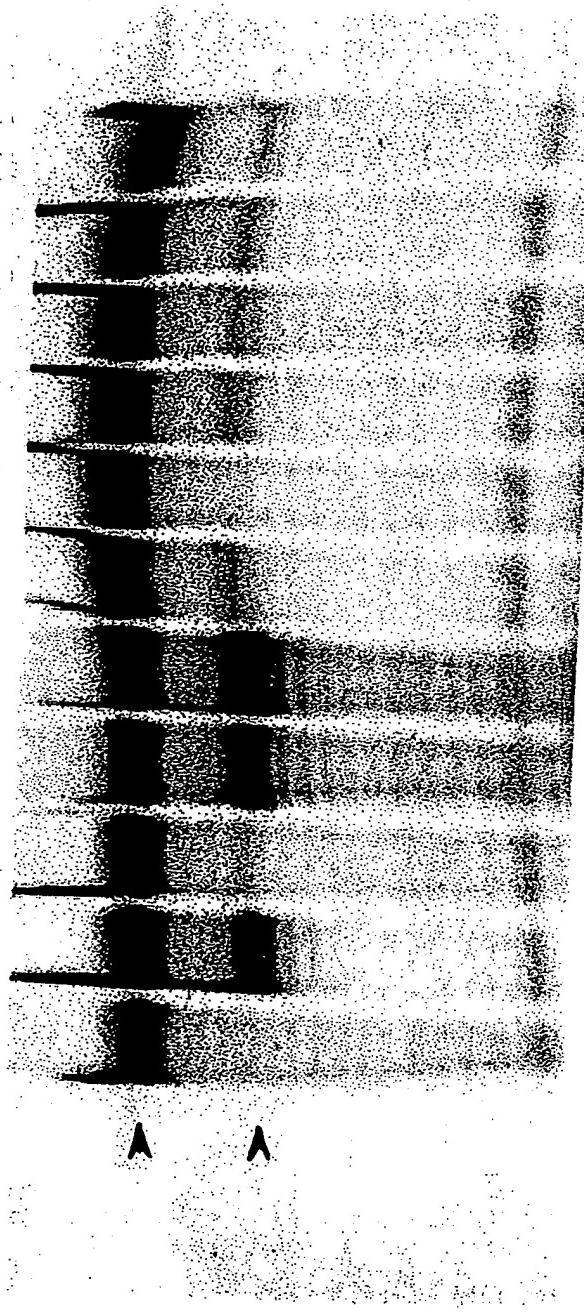
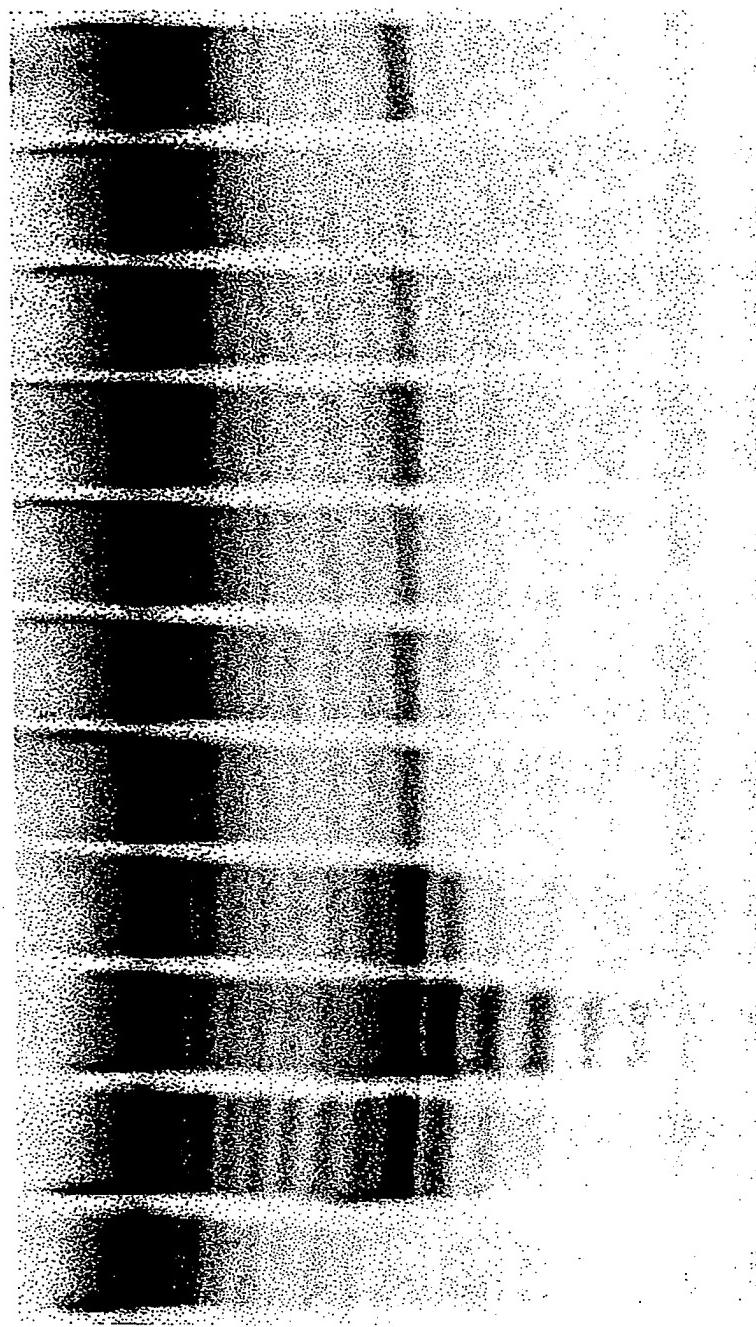


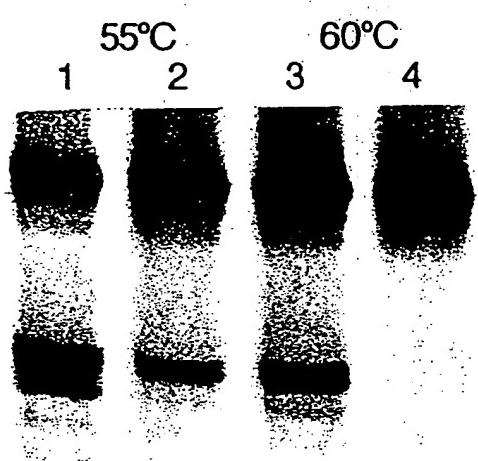
FIGURE 38 32E+1200T

1 2 3 4 5 6 7 8 9 10 11



50

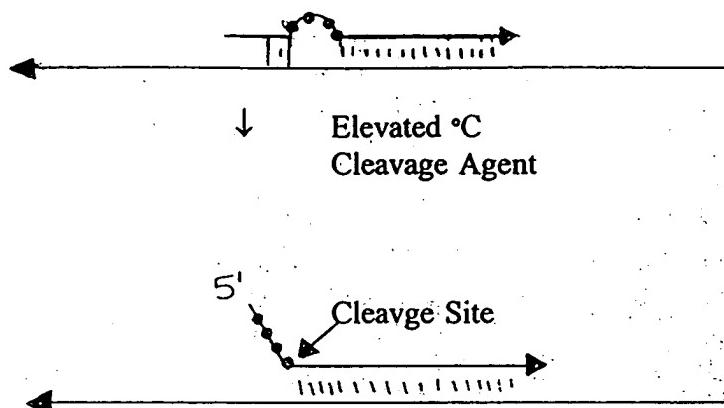
**FIGURE 39**



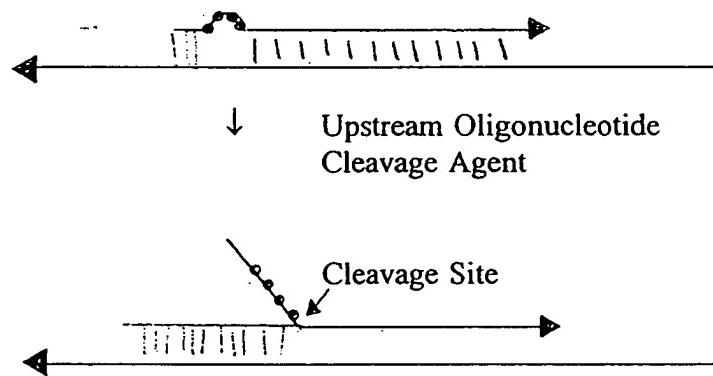
2007-02-12

FIGURE 40

a.



b.



52

正四十二卷

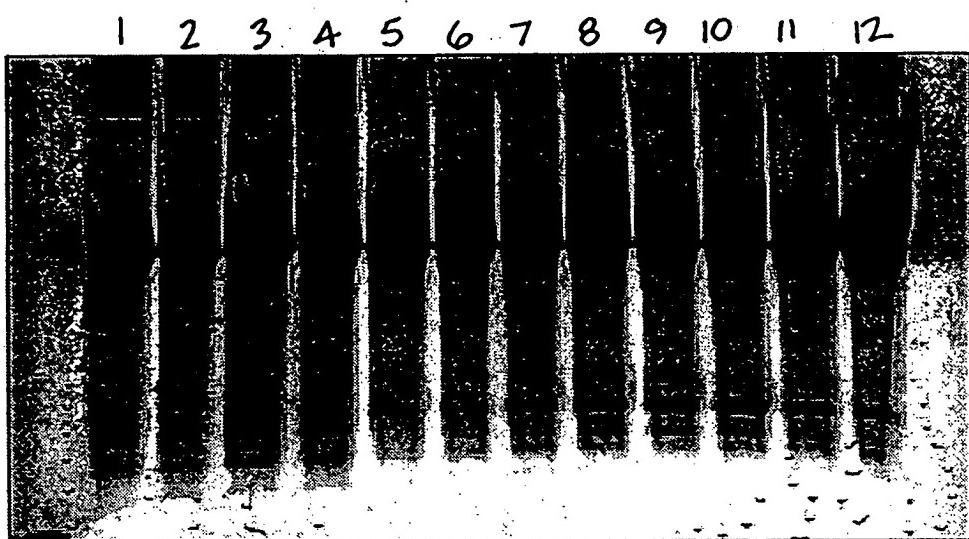
FIGURE 41

## Invasive Cleavage Directing Oligo

cleavage site

1

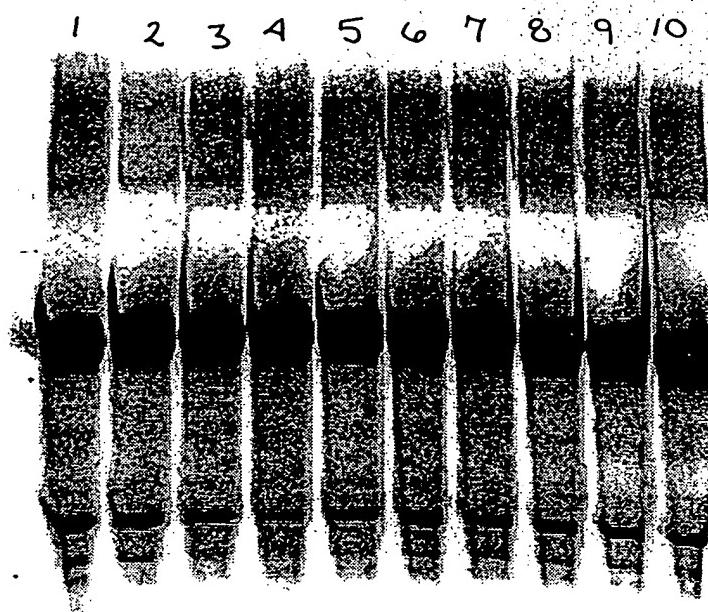
**FIGURE 42**



10074328 - 023202

54

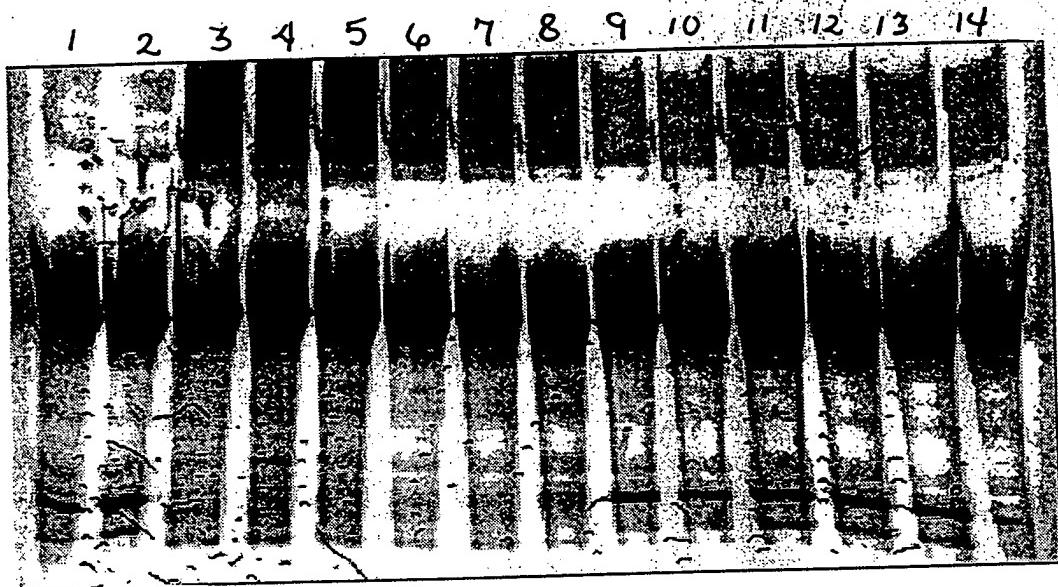
**FIGURE 43**



400ア4328 "021202

55

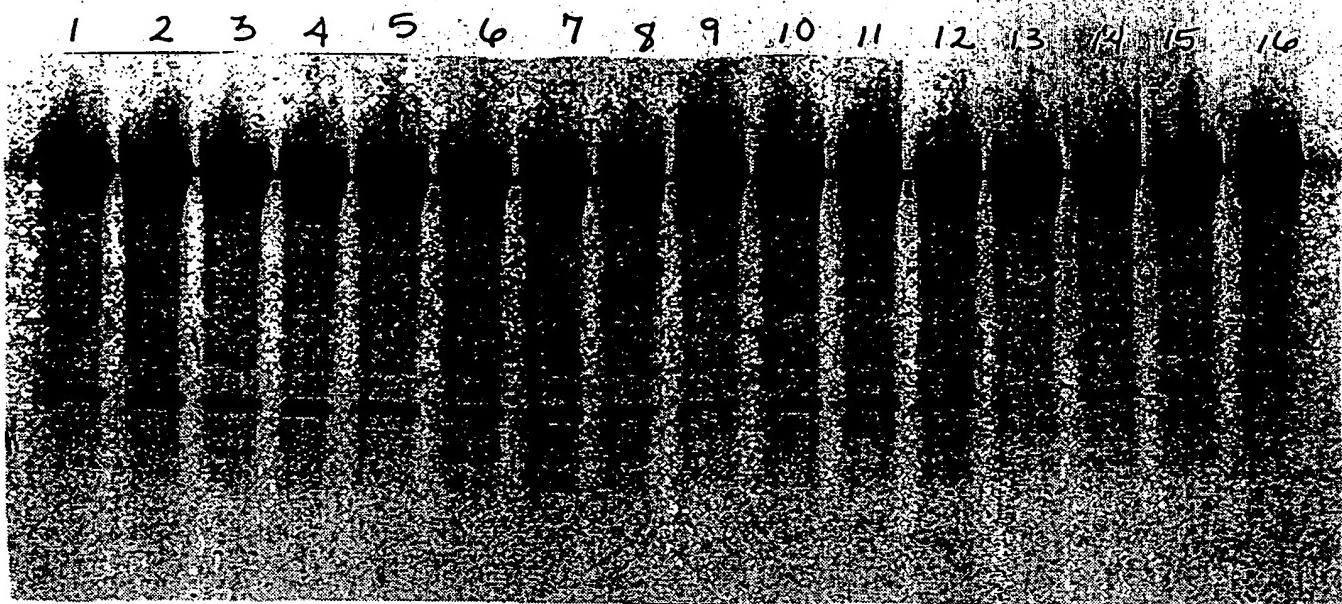
**FIGURE 44**



10074328 "021202

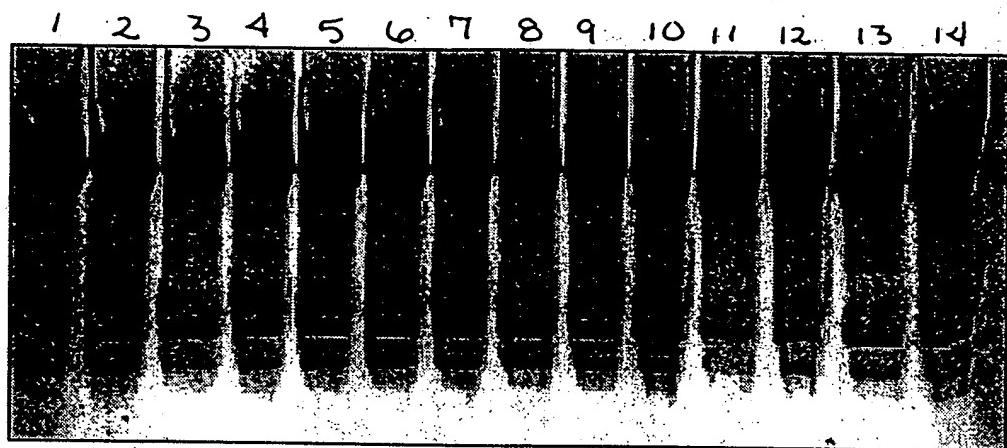
56

**FIGURE 45**



57

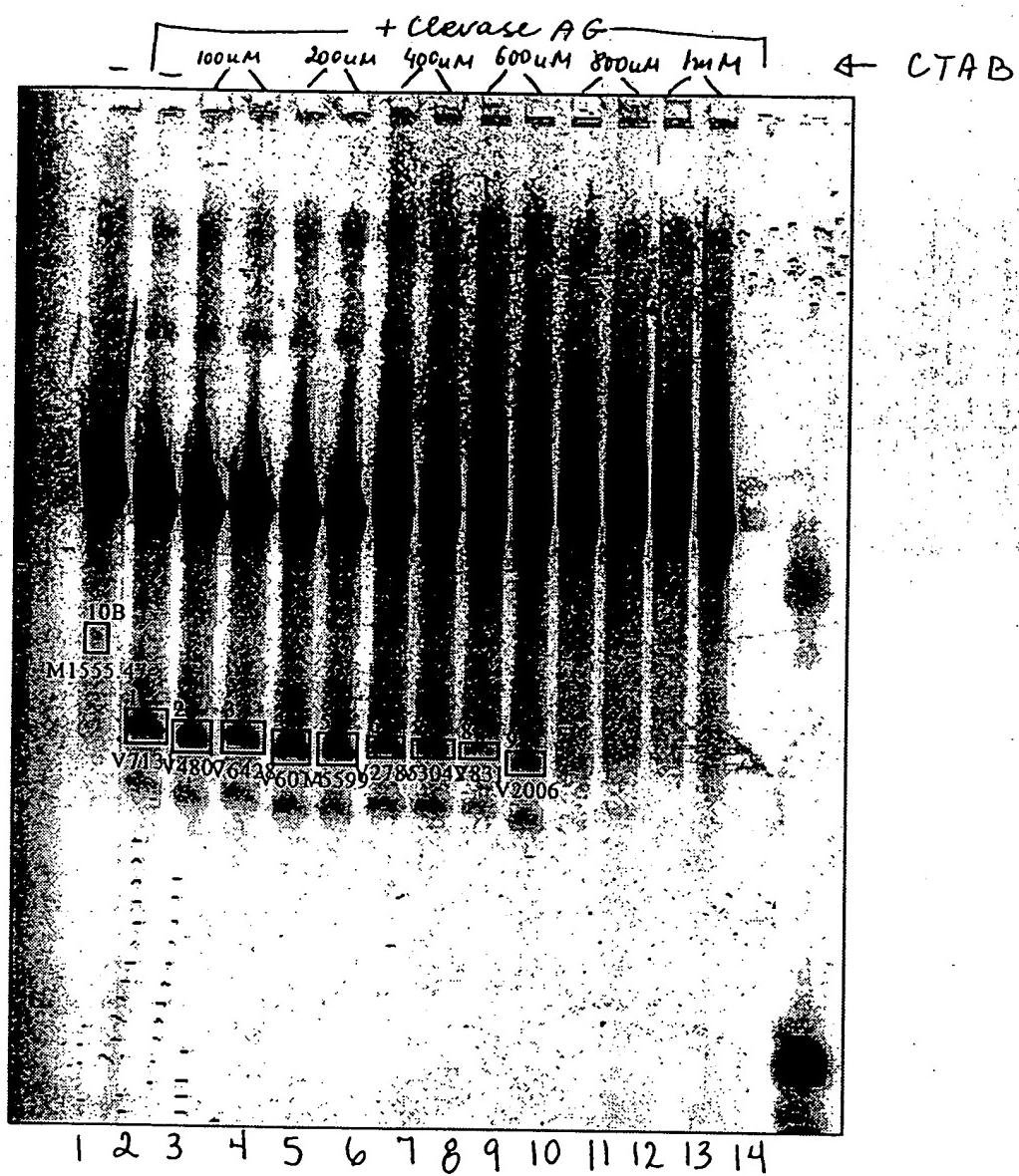
**FIGURE 46**



40074326 021202

58

FIGURE 47



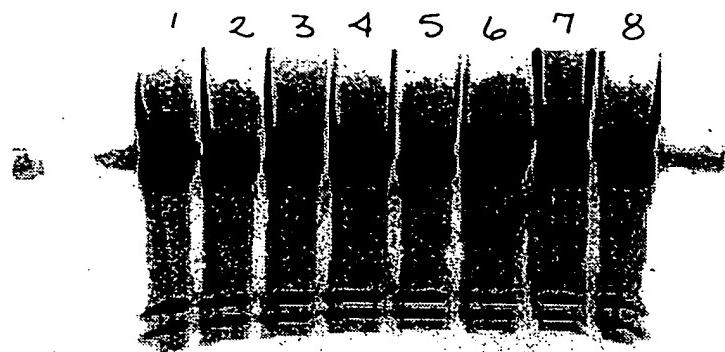
59

**FIGURE 48**



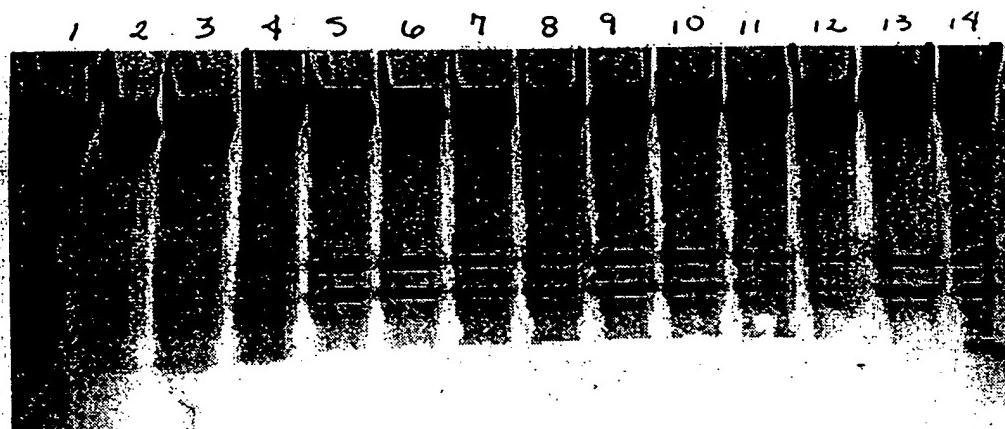
100アメニティ

**FIGURE 49**



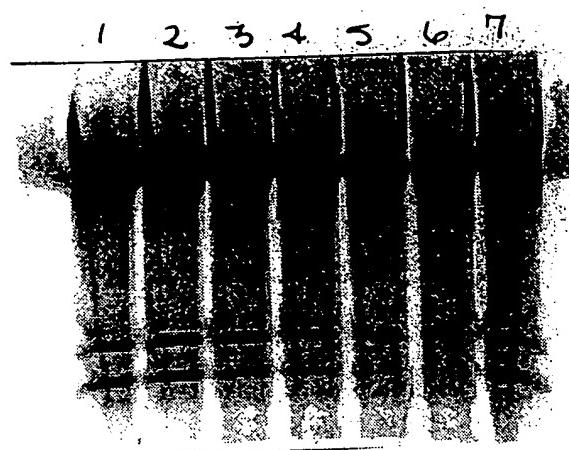
20074328 "021202

FIGURE 50



100ア4328 "021202

**FIGURE 51**



10074328 "021203

63

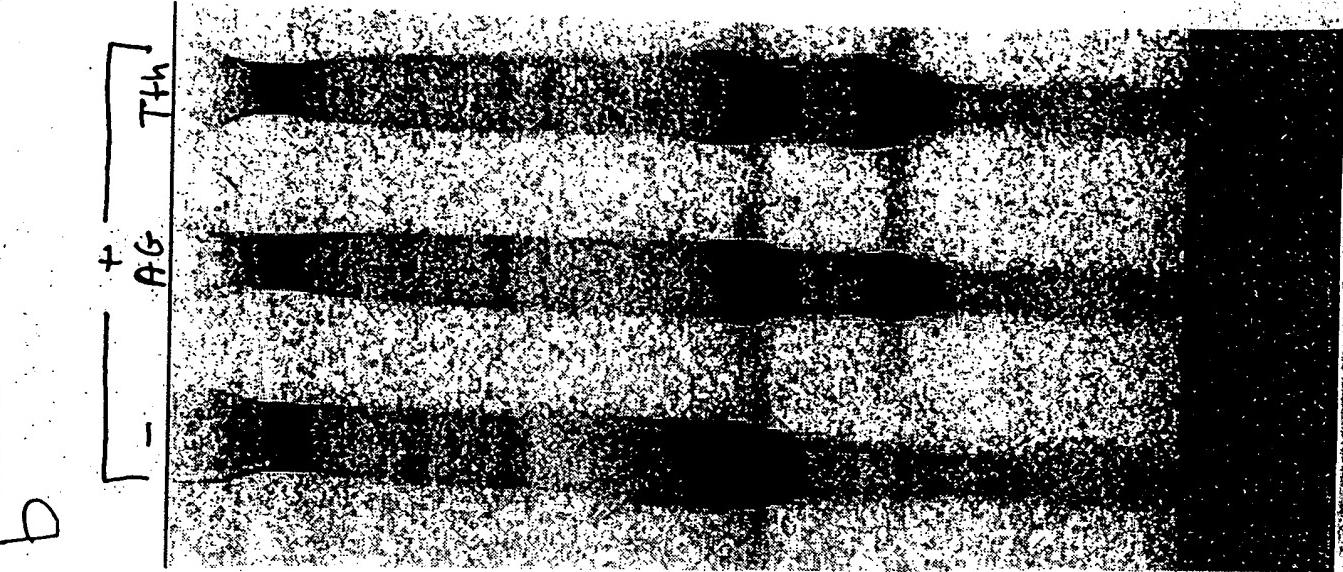
**FIGURE 52**



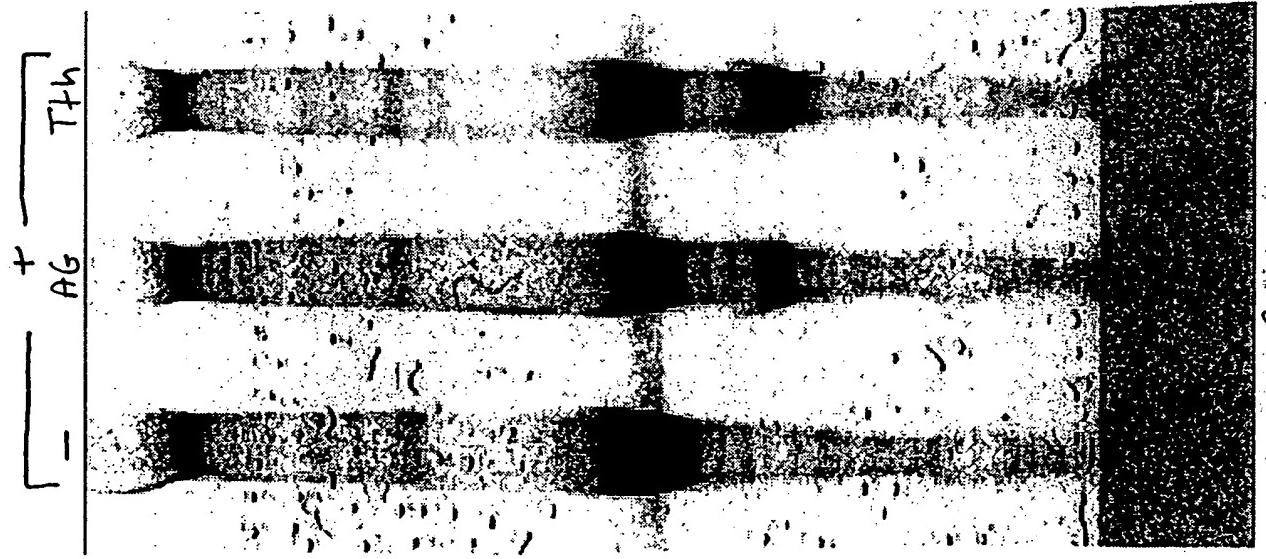
40074328 "021202

64

FIGURE S3



a



TARGET RNA →

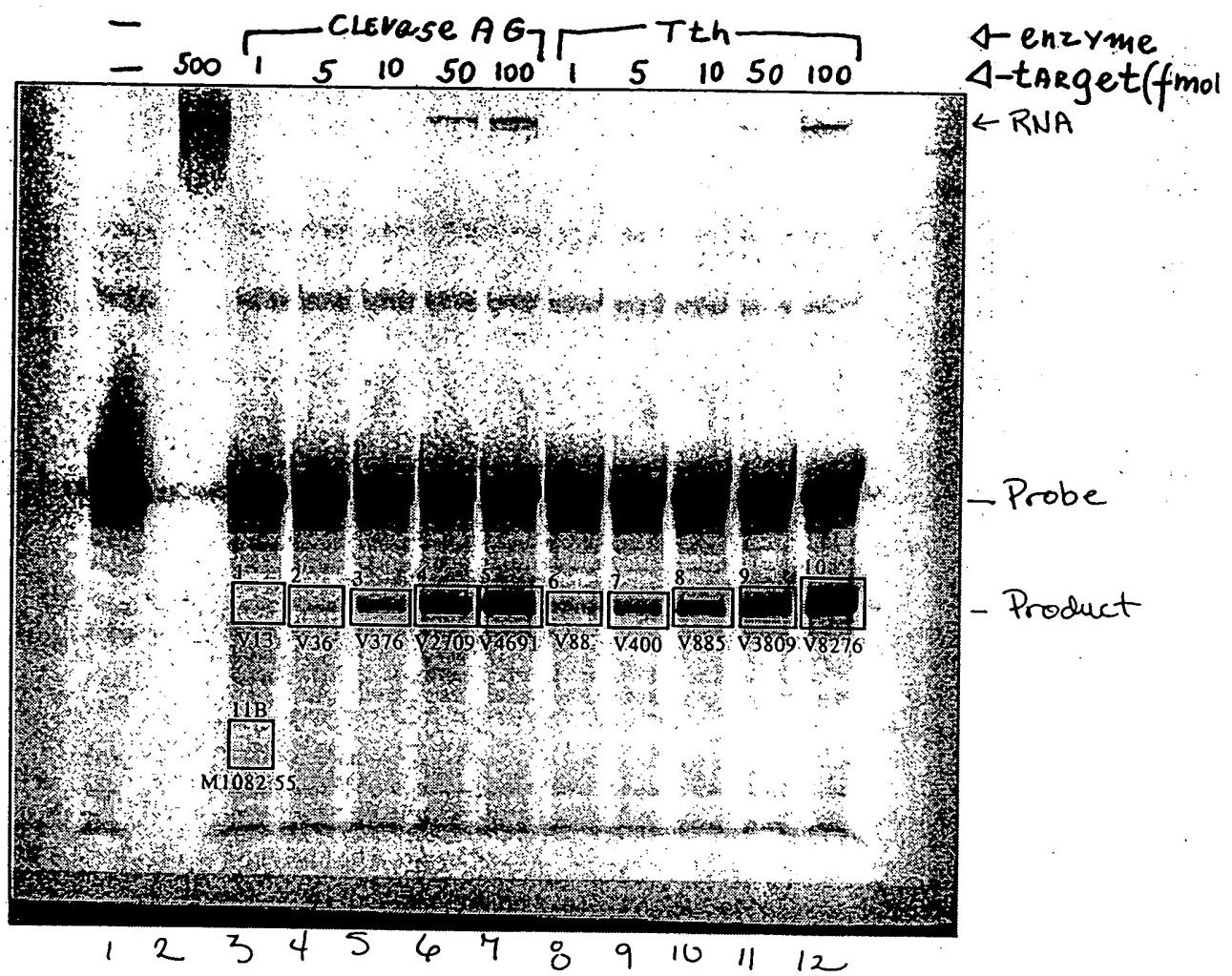
Uncleaved  
Probe →

Cleaved  
Probe →

65

FIGURE 54

10004328 "021202



**FIGURE 55**



67

FIGURE 56

70 (C10 amino T's)  
74 (C6 amino T's)

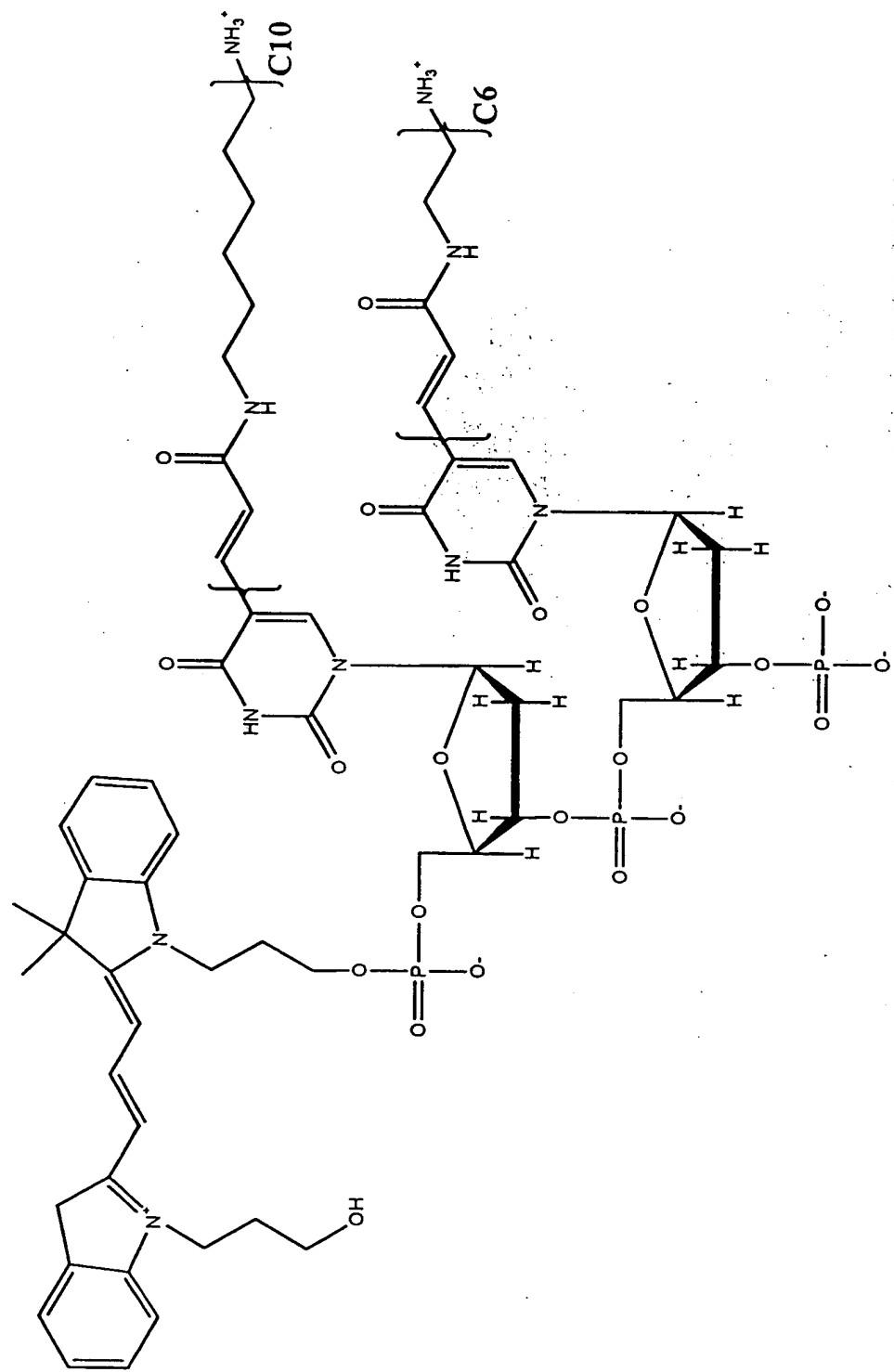
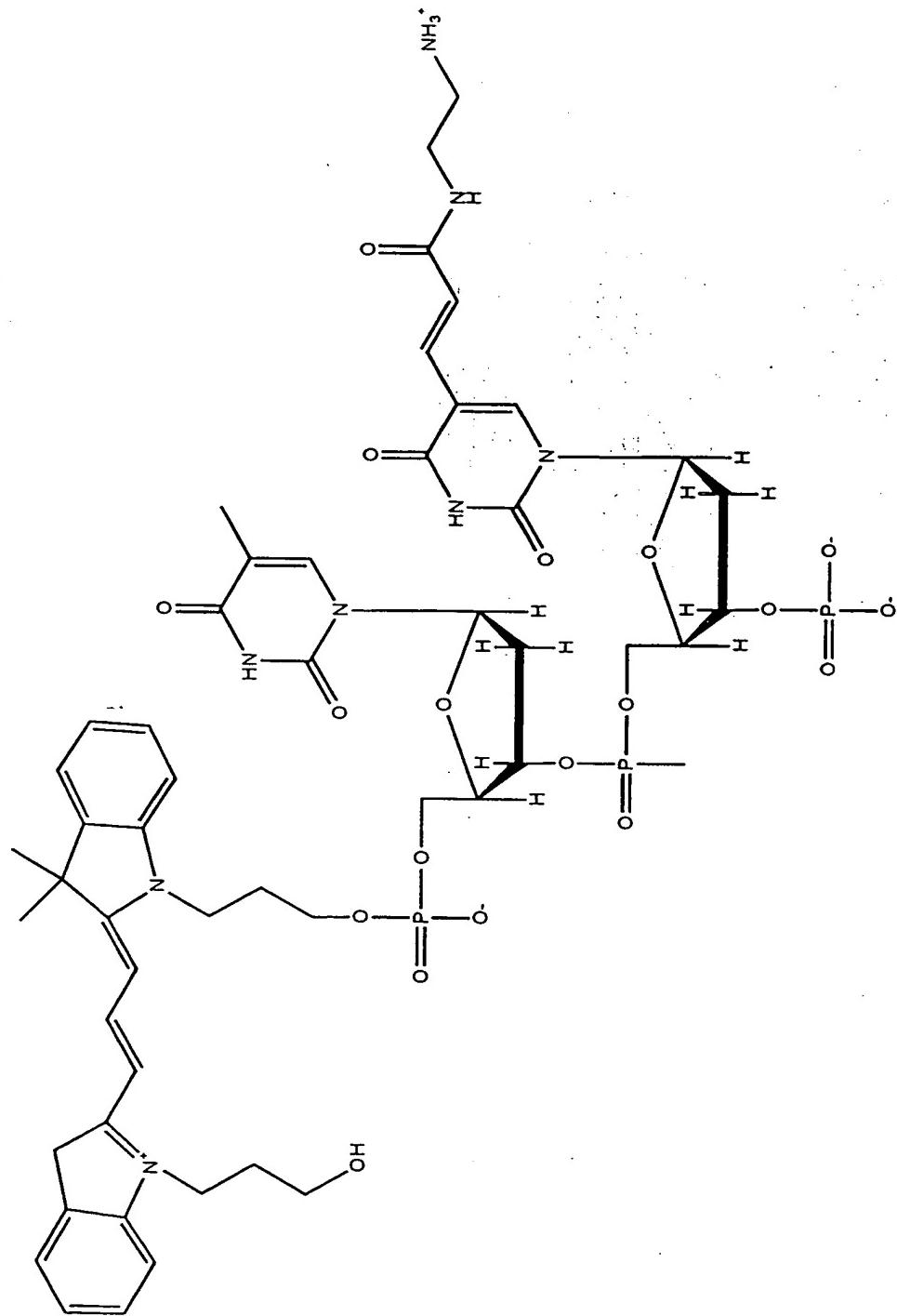


FIGURE 57 2227-200

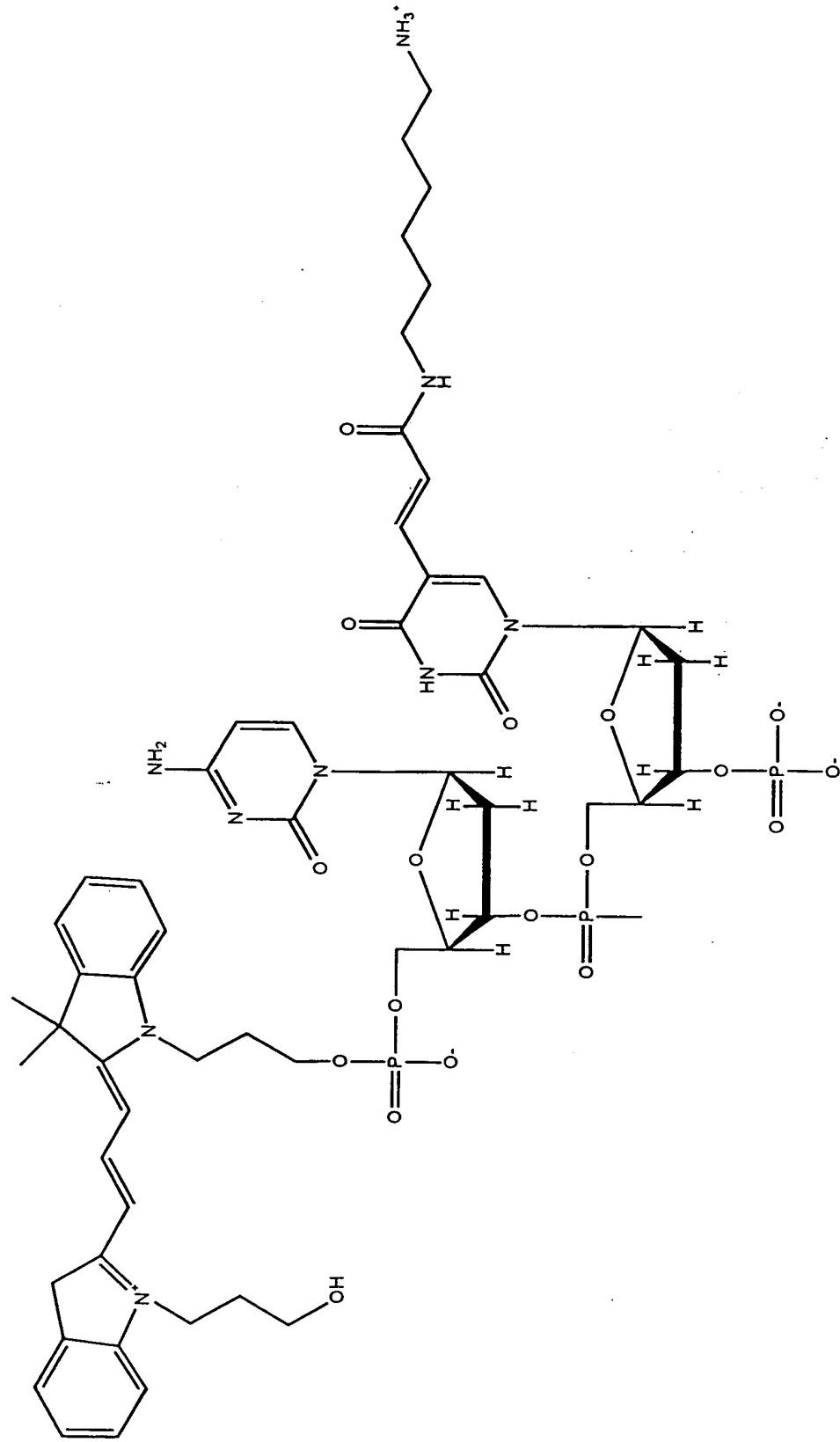
75



69

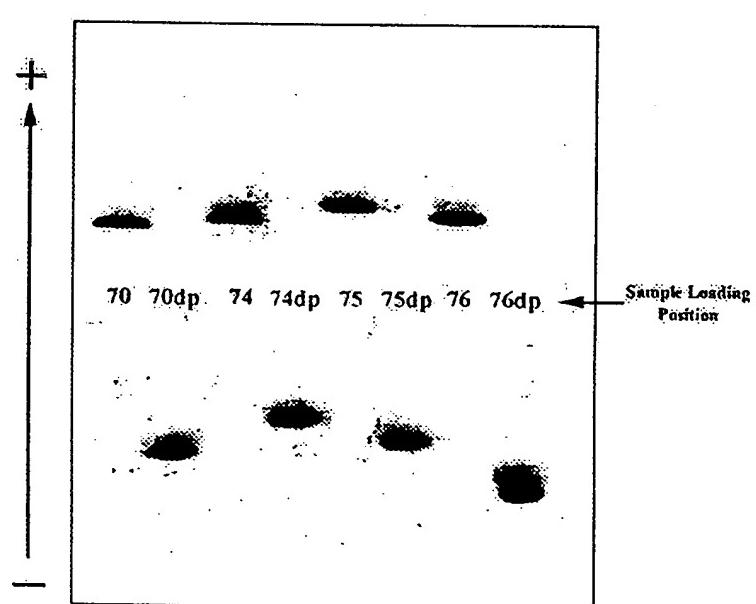
202520 "SCE-43400T  
FIGURE 58

76



76

**FIGURE 59**

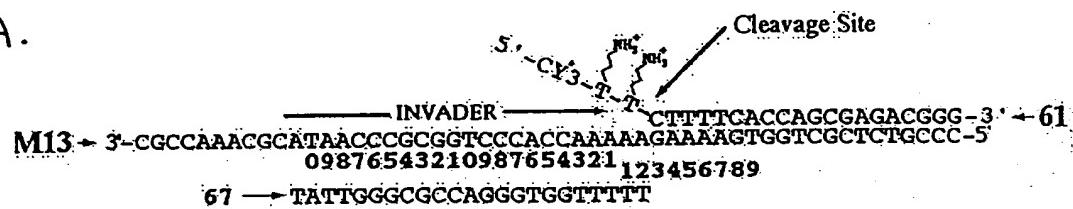


10074328 "021202

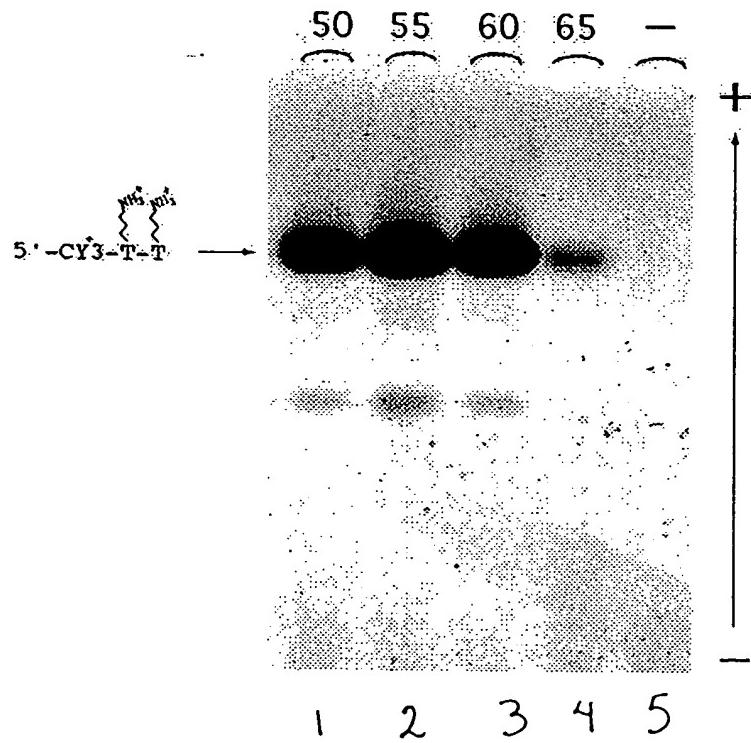
71

FIGURE 60

A.



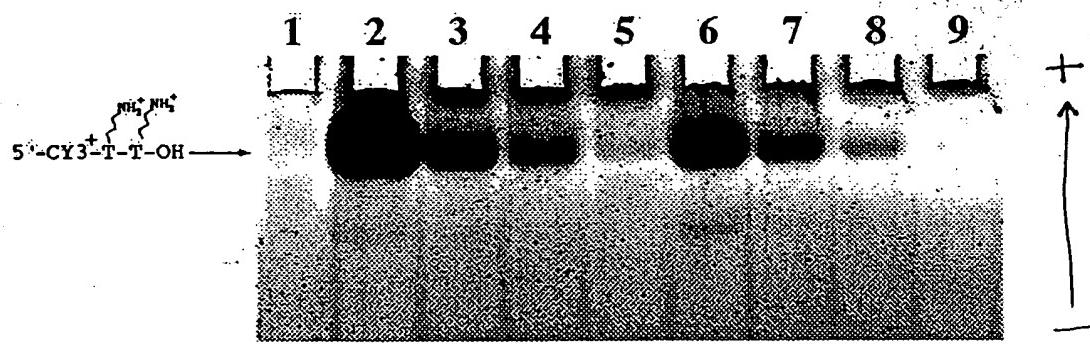
B.



72

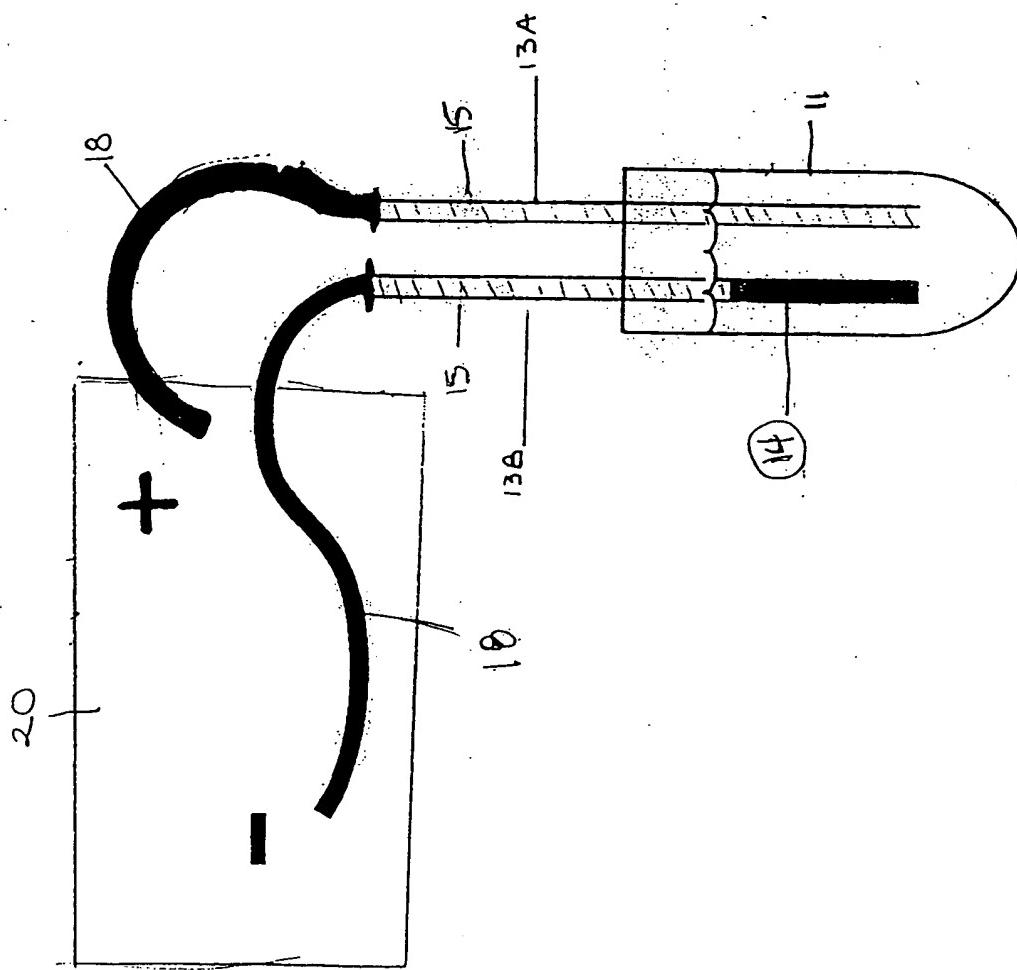
10074328-021202

**FIGURE 61**



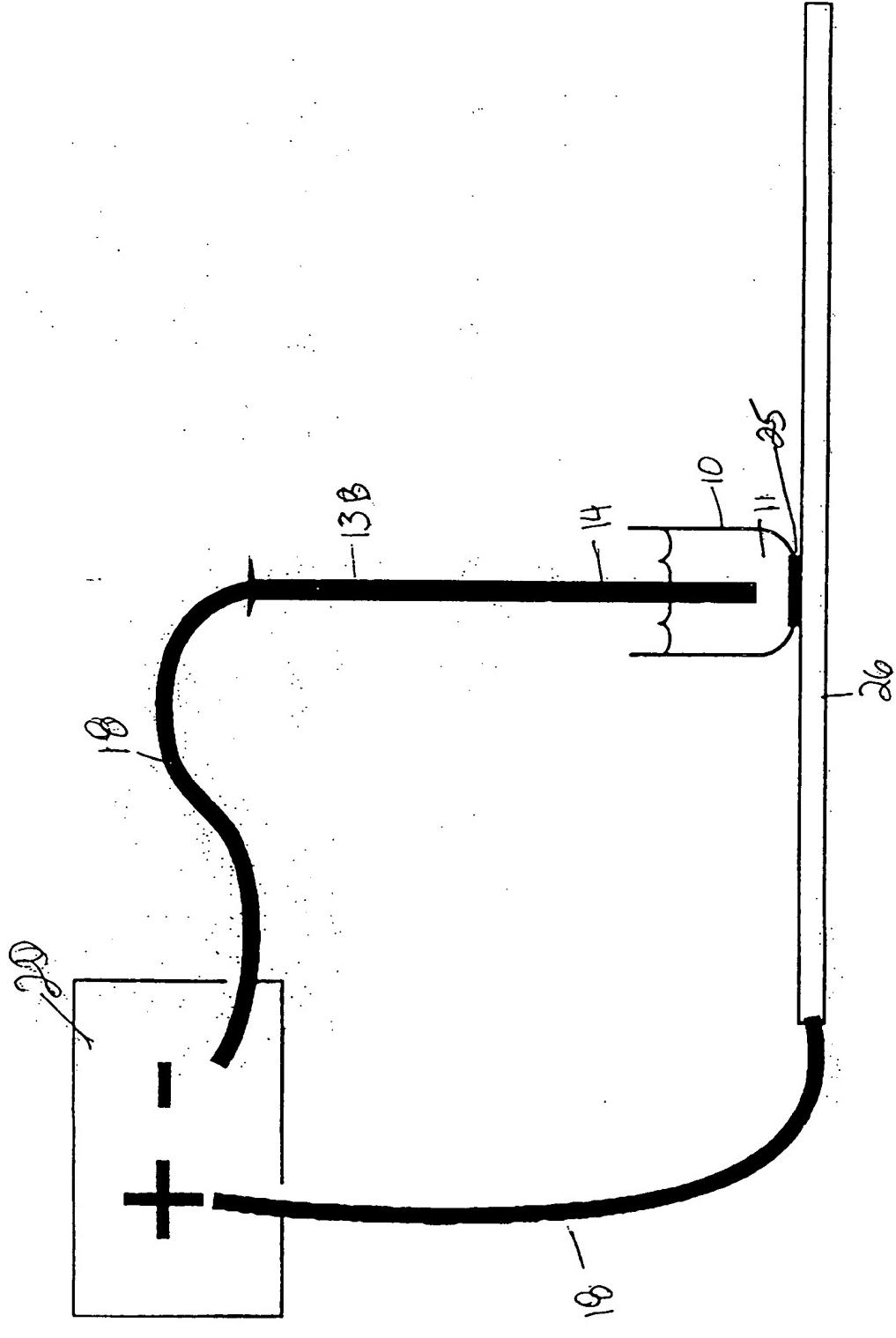
202720 " Sample 200T

FIGURE 62



20210 " EETIXQOT

FIGURE 63



75

FIGURE 64

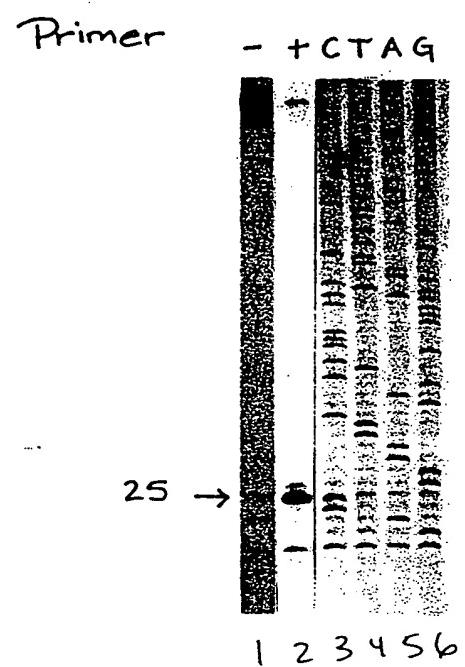


FIGURE 65

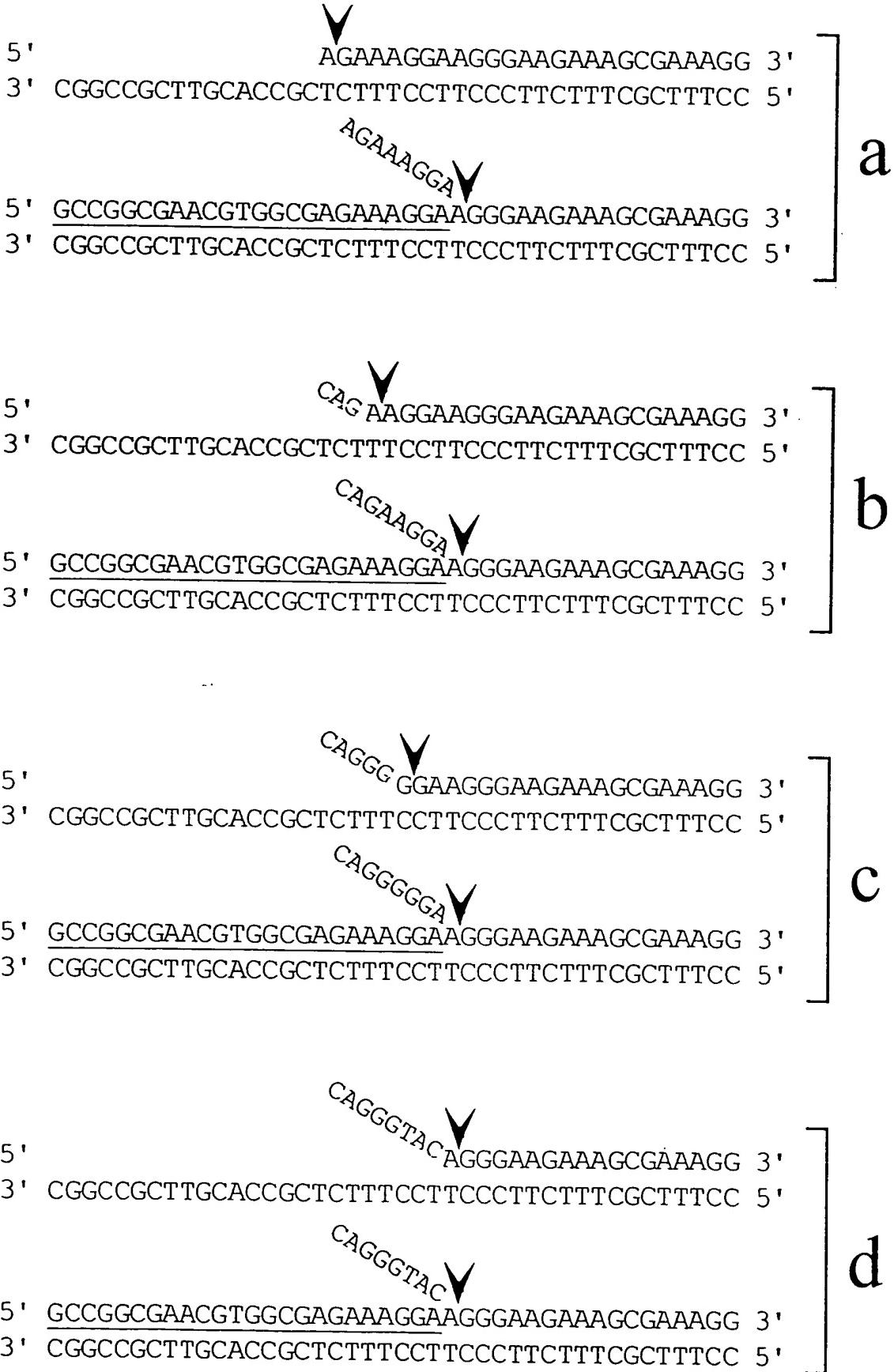


FIGURE 66

